

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 30, 2001, 19:41:24, Sequence: 100% of Sequences  
(without alignments)

7,576 Million cell updates/sec

Title: US-09-498-556-85

Perfect score: 4 XXXX 4

Sequence: 1 XXXX 4

Scoring table: HLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 412676 seqs, 666,444K residues

Total number of hits satisfying chosen parameters: 412,76

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A.Geneseq.0601:\*

1: /SIDS8/qcdat4a/geneseq/geneseq/AA1980.DAT:\*

2: /SIDS8/qcdat4a/geneseq/geneseq/AA1981.DAT:\*

3: /SIDS8/qcdat4a/geneseq/geneseq/AA1982.DAT:\*

4: /SIDS8/qcdat4a/geneseq/geneseq/AA1983.DAT:\*

5: /SIDS8/qcdat4a/geneseq/geneseq/AA1984.DAT:\*

6: /SIDS8/qcdat4a/geneseq/geneseq/AA1985.DAT:\*

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8: /SIDS8/qcdat4a/geneseq/geneseq/AA1987.DAT:\*

9: /SIDS8/qcdat4a/geneseq/geneseq/AA1988.DAT:\*

10: /SIDS8/qcdat4a/geneseq/geneseq/AA1989.DAT:\*

11: /SIDS8/qcdat4a/geneseq/geneseq/AA1990.DAT:\*

12: /SIDS8/qcdat4a/geneseq/geneseq/AA1991.DAT:\*

13: /SIDS8/qcdat4a/geneseq/geneseq/AA1992.DAT:\*

14: /SIDS8/qcdat4a/geneseq/geneseq/AA1993.DAT:\*

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20: /SIDS8/qcdat4a/geneseq/geneseq/AA1999.DAT:\*

21: /SIDS8/qcdat4a/geneseq/geneseq/AA2000.DAT:\*

22: /SIDS8/qcdat4a/geneseq/geneseq/AA2001.DAT:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	FR	ID	Description
1	0	0.0	1	20	AA446652	Immunogenic peptide
2	0	0.0	2	2	AA10185	Sequence of synthe
3	0	0.0	2	6	AA50013	Sequence linking 1
4	0	0.0	2	8	AA70513	Sequence of somato
5	0	0.0	2	18	AA17544	beta-A1-crystallin
6	0	0.0	2	21	AA63093	Human secreted pro
7	0	0.0	2	21	AA37326	Human secreted pro
8	0	0.0	2	21	AA39141	Human secreted pro
9	0	0.0	2	21	AA44709	Human secreted pro
10	0	0.0	2	21	AA44925	Human secreted pro
11	0	0.0	2	21	AA44451	Human secreted pro

12	0	0.0	2	21	AA627796	Human secreted pro
13	0	0.0	2	21	AA627827	Human secreted pro
14	0	0.0	2	21	AA627830	Human secreted pro
15	0	0.0	2	21	AA627834	Human secreted pro
16	0	0.0	2	21	AA634601	Human secreted pro
17	0	0.0	2	21	AA634615	Human secreted pro
18	0	0.0	2	21	AA49410	Novel autism pepti
19	0	0.0	2	22	AA66466	Human secreted pro
20	0	0.0	3	2	AA101301	Sequence which cor
21	0	0.0	3	2	AA10296	(A1a)3 Daumoycin
22	0	0.0	3	2	AA10297	Lytyllys-Daumoyc
23	0	0.0	3	3	AA20375	Analgesic peptide
24	0	0.0	3	4	AA330601	Sequence of beta-1
25	0	0.0	3	4	AA30457	Sequence of collagen
26	0	0.0	3	5	AA40819	Sequence of frame
27	0	0.0	3	6	AA50012	Sequence linking 1
28	0	0.0	3	7	AA60186	Renin-inhibitor pe
29	0	0.0	3	9	AA62709	Renin-inhibitory p
30	0	0.0	3	9	AA61081	Sequence encoded b
31	0	0.0	3	10	AA60082	Binding receptor w
32	0	0.0	3	10	AA61660	Synthetic peptide
33	0	0.0	3	10	AA63533	N-terminal portion
34	0	0.0	3	10	AA63348	Portion of myc var
35	0	0.0	3	10	AA60663	New antihypertensi
36	0	0.0	3	10	AA60664	New antihypertensi
37	0	0.0	3	10	AA60665	New antihypertensi
38	0	0.0	3	10	AA60667	New antihypertensi
39	0	0.0	3	10	AA60668	New antihypertensi
40	0	0.0	3	10	AA60678	New antihypertensi
41	0	0.0	3	10	AA62798	Sequence of frame
42	0	0.0	3	10	AA62811	Sequence of frame
43	0	0.0	3	11	AA60457	Antiviral agent
44	0	0.0	3	11	AA60797	Low toxicity immun
45	0	0.0	3	21	AA79636	Peroxidase reactan

#### ALIGNMENTS

RESULT 1	
AA446652	Standard: Peptide: 1 AA
AA446652	
AA446652	
01-DEC-1999	(first entry)
Immunogenic peptide having a human leukocyte antigen binding motif #1563.	
Human leukocyte antigen binding, immunogenic, glycoprotein, MHC: HLA:	
Cytotoxic T lymphocyte cell tumor rejection, viral infection, cancer:	
prostate cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma;	
vaccine; immunisation.	
Synthetic.	
Homo sapiens.	
W09945954-A1.	
16-SEP-1999.	
13-MAR-1998:	98WO-0505039.
13-MAR-1998:	98WO-0505039.
(EPIM- ) EPIMUNE INC.	
Sette A, Kato PT, Sjöberg L, Collis F, Grey HM, Crawford S:	
WPL: 1999-551214/46.	
New immunogenic peptides with HLA binding motif, useful in treatment	

PT and diagnosis of cancers and viral diseases -  
 XX  
 PS claim 1; Page 80; 150pp; English.  
 XX  
 CC AAV4540 to AAV44214 represent specifically claimed immunogenic peptides  
 CC having a human major histocompatibility complex (MHC) Class I (also  
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic  
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes  
 CC HLA A2.1, A1, A2.2 or A24.1 or HLA B or C) and induce a cytotoxic T cell  
 CC response against the antigen from which the peptide is derived.  
 CC cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are  
 CC normally induced by an antigen in the form of a peptide fragment bound  
 CC to a HLA molecule, rather than the intact foreign antigen itself, and  
 CC are particularly important in tumour rejection and in fighting viral  
 CC infections. The peptides are therefore useful therapeutically to treat  
 CC or prevent viral infections and cancers in mammals (especially humans)  
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.  
 CC They can be administered as vaccines to elicit an immune response in  
 CC individuals susceptible or otherwise at risk of viral infection or  
 CC cancer, or used to treat chronic or acute conditions. They are also  
 CC useful diagnostically, and can be used to induce a cytotoxic T cell  
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to  
 CC produce CTLs ex vivo for infusion back into a patient. The  
 CC polypeptides encoding the immunogenic peptides are also useful  
 CC therapeutically and for immunisation as above.  
 XX  
 SO Sequence 1 AA:  
  
 Query Match 0.0%; Score 0; 18 20; Length 1;  
 Best Local Similarity 0.0%; Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 X 1  
 DB 1 y 1  
  
 RESULT 2  
 AAF10185  
 ID AAF10185 standard; Protein; 2 AA.  
 XX  
 AC AAF10185;  
 XX  
 DE 14-AUG-1992 (first entry)  
 DE  
 DE Sequence of synthetic polypeptide for the produ. of aspartame.  
 XX  
 KM Aspartyl-phenylalanine methyl ester; artificial sweetener;  
 KM aspartame.  
 XX  
 PN EP 6258-A.  
 XX  
 PD 24 SEP-1981.  
 XX  
 PF 02-MAR-1981; 81EP-0300857.  
 XX  
 PK 14-MAR-1980; 800S-010462.  
 XX  
 PA (CETU ) CETUS CORP.  
 XX  
 PI rose JF, White LD, Bahl CP;  
 XX  
 DR WPI: 1981-721340/40.  
 DR N-PSDB; AAN10059.  
 XX  
 PT Aspartame prenu. from synthetic polypeptide - produced by cloned  
 PT microorganism  
 XX  
 PS Disclosure; Page 5; 18pp; English.  
 XX  
 CC The inventors claim a method for the produ. of aspartame by first  
 CC synthesising double-stranded DNA in which a coding strand has

CC alternating codings for Asp and the Phe in sufficient number to  
 CC produce a polypeptide which is stable in pre-determined host  
 CC microorganisms. The DNA strand is then inserted into a cloning  
 CC vehicle so that the resulting chimera directs the synthesis of the  
 CC Asp protein. This protein is then cleaved with CNBr or trypsin  
 CC to release the peptide which, after benzoylation, can be fragmented  
 CC by digestion with cyanoethylpsin.  
 XX  
 SO Sequence 2 AA:  
  
 Query Match 0.0%; Score 0; 18 2; Length 2;  
 Best Local Similarity 0.0%; Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 X 1  
 DB 1 d 1  
  
 RESULT 3  
 AAF50013  
 ID AAF50013 standard; Protein; 2 AA.  
 XX  
 AC AAF50013;  
 XX  
 DE 03-SEP-1991 (first entry)  
 DE  
 DE Sequence linking insulin B chain B(1-29) to A chain a(1-21) to form  
 DE a biosynthetic insulin precursor.  
 XX  
 DE Insulin precursor; diabetes; proteolysis resistant.  
 XX  
 FE Key location/qualifiers  
 FT Misc-difference 1 /note- "attached to B(1-29)"  
 FT FT  
 FT Misc-difference 2 /note "attached to A(1-21)"  
 XX  
 PN EP16329-A.  
 XX  
 PD 04-DEC-1985.  
 XX  
 PF 29-MAY-1985; 85EP-0116297.  
 XX  
 PK 08-FEB-1985; 85DK-0000582.  
 PR 30-MAY-1984; 84DK-0002665.  
 PR 29-MAY-1985; 85DK-0002385.  
 PR 15-NOV-1990; 90EP-0121887.  
 XX  
 PA (NOVO ) NOVO INDUSTRIAL A/S.  
 XX  
 PI Marussen J, Fild N, Ammerer G, Hansen M, Thim L, Norris K;  
 PI Voigt BO;  
 XX  
 DR WPI: 1985-104970/49.  
 XX  
 PT DNA sequence encoding insulin precursor having correctly  
 PT positioned disulphide bridges and resistant to proteolytic degradation  
 XX  
 PS Claim 5; Page 32; 47pp; English.  
 XX  
 CC The biosynthetic insulin precursors are generated largely with  
 CC correctly positioned disulphide bridges between the A- and B-  
 CC moieties, and are more resistant to proteolytic degradation than  
 CC previously.  
 XX  
 SO Sequence 2 AA:  
  
 Query Match 0.0%; Score 0; 18 6; Length 2;  
 Best Local Similarity 0.0%; Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1  
DB 1 s 1

RESULT 4  
AAP70513  
ID AAP70513 standard; protein; 2 AA.

AC AAP70513;  
XX 19-JAN-1991 (first entry)

DE Sequence of somatostatin encoded by a portion of pscm1-3.

KW Microbial cloning vector; gene expression.

XX Key Location/Qualifiers

FT Misc-difference 2 /note="AA no. 1"

XX US4704362 A.

XX 03-NOV-1987.

XX 05-NOV-1979; 79US-0090979.

XX 05-NOV-1979; 79US-0090979.

XX (GETH ) GENENTECH INC.

XX Itakura K, Riggs AD;

XX WPI; 1987-327630/45.

XX N-PSD; AAN70854.

XX Recombinant DNA cloning vehicle comprising a low-copy control region and a DNA insert coding for a functional heterologous polypeptide.

XX Example; Fig 5B; 24pp; English.

XX The EcoRI PstI fragment of the pscm1 (AAN70853) with the lac-controlling element was removed and replaced with the EcoRI-PstI

XX fragment of pBP122 to place pscm1. The EcoRI fragment of

XX lambda-phage 5, carrying the lac operon control region and most of

XX the beta-galactosidase structural gene was inserted into the EcoRI

XX site of pscm1. Analysis of isolated clones for somatostatin

XX activity then identified clones carrying the properly oriented gene

XX of which pscm1-3 (AAN70854; AAN70855) was one which produced

XX somatostatin on cyanogen bromide treatment. 1003 AAs separate the

XX C-terminal of AAP70513 from the N-terminal of AAP70514.

XX Sequence 2 AA;

XX

XX

XX

XX

XX

XX

XX

XX

XX Beta-A3-crystallin N-terminal peptide analogue T31.  
DE  
XX Beta-A3-crystallin, lens protein; cataract; antigen; autoimmune;  
KW epithelial cell; epitope.  
XX  
XX Synthetic.  
OS Homo sapiens.  
XX

XX Key Location/Qualifiers

FT Misc-difference 3 /note="Thr has been replaced by Ile"

XX EP770398-A2.

XX 02-MAY-1997.

XX 10-OCT-1996; 96EP-0116212.

XX 13-OCT-1995; 95JP-0291993.

XX (SENP ) SENJU PHARM CO LTD.

XX Inoue E;

XX WPI; 1997-237935/22.

XX Composition containing lens antigen of microorganism that expresses

XX it, used to treat or prevent cataract by reducing the level of

XX antibodies directed against lens protein

XX Example 3; Page 20; 38pp; English.

XX Peptides constituting beta-A3-crystallin were synthesised and

XX subjected to competitive inhibition assay of beta-A3-crystallins and

XX respective oligopeptides. As a result, only the N-terminal peptide

XX fragment showed a strong binding inhibitory effect on beta-A3-crystallin

XX This suggests that the binding site (epitope) of beta-A3-crystallin to

XX the antibody was present in the N-terminal 6 amino acid residues.

XX To identify the minimum unit of epitope, one residue of six amino acid

XX residues of the N terminal sequence MTQAE was substituted by isoleucine

XX to give six kinds of analogues. The present sequence has residue

XX 3 substituted by isoleucine. Only the peptide-IFTQAE showed a strong

XX inhibitory effect on beta-A3-crystallin, suggesting that the

XX sequence EFTQAE was the epitope of beta-A3-crystallin. Lens antigens of

XX microorganism that can express a lens antigen are used in a

XX pharmitic test composition. The composition can be used to prepare

XX an inhibitor of an increase of anti-lens protein antibodies. The

XX composition and the inhibitor can be used to treat, prevent or delay the

XX onset of cataract. Cataract is considered to be the result of autoimmune

XX damage to lens epithelial cells induced by lens protein.

XX Sequence 2 AA;

XX

XX

XX

XX



KM anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; antileish-  
 KM manary; antileishmanial; antibacterial; antileishmanial; antileishmanial;  
 KM cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
 KM neurological disease; infection; human; secreted protein.  
 OS  
 XX Homo sapiens.  
 XX  
 PN W0200058513-A1.  
 XX  
 PD 05-OCT-2000.  
 XX  
 PE 22-MAR-2000; 2000WO-0507506.  
 XX  
 PR 26-MAR-1999; 99US-0126507.  
 XX  
 PR 17-OCT-1999; 99US-0172412.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI (POSEF) POSEF C A  
 XX  
 PI Rosen CA, Rubin SM, Komatsoulis G;  
 XX  
 DR WPI: 2000-544644/56.  
 DR N-PSDB: AAC73913  
 XX  
 FT Fully active polypeptide sequences, and their secreted  
 PT polypeptides, used in the treatment and diagnosis of cancers,  
 PI autoimmune disorders, and skin disorders.  
 XX  
 PS Claim 11: Page 387; 413pp; English.  
 XX  
 CC Sequences AAH39043-R39141 represent the amino acid sequences of 49  
 CC human secreted proteins encoded by the genes AAC73905-R3913. The genes  
 CC and proteins are useful for preventing, ameliorating or treating medical  
 CC conditions, e.g. by protein or gene therapy. The genes are isolated from  
 CC a range of human tissues disclosed in the specification. The nucleic  
 CC acids, proteins, antibodies and (ant)ipeptides are used in the  
 CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone  
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
 CC hemolytic anemia, autoimmune thyroiditis, diabetes mellitus,  
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and osteoporosis;  
 CC (c) cardiovascular disorders such as myocardial ischemia and  
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
 CC and parasite infections.  
 CC  
 XX Sequence 2 AA:  
 SQ  
 Query Match 0.0%; Score 0; DB 21; Length 2;  
 Best local similarity 0.0%; Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0.  
 QY 1 X 1  
 Db 1 p 1  
 DE Human secreted protein sequence encoded by gene 15 SEQ ID NO:75.  
 XX  
 XX Human secreted protein; diagnosis; anti-allergic; immunosuppressive;  
 KM anti-inflammatory; antiproliferative; cytostatic; cardiant; vasotropic;  
 KM cerebroprotective; nociceptive; neuroprotective; antibacterially; virucide;  
 KM fungicide; ophthalmological; viderary; gene therapy; autoimmune disease;

KM hyperproliferative disorder; cardiovascular disorder; angiogenesis;  
 KM cerebrovascular disorder; nervous system disorder; infection;  
 KM wound healing; food additive; preservative; skin aging.  
 OS  
 XX Homo sapiens.  
 XX  
 PN W0200058494-A1.  
 XX  
 PD 05-OCT-2000.  
 XX  
 PE 23-MAR-2000; 2000WO-0507578.  
 XX  
 PR 26-MAR-1999; 99US-0126507.  
 XX  
 PR 07 JAN 2000; 2000US-0174672.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Rubin SM, Komatsoulis G;  
 XX  
 DR WPI: 2000-544644/56.  
 DR N-PSDB: AAC79754.  
 XX  
 FT New nucleic acid molecules encoding 50 human secreted proteins for  
 PT diagnosis, prevention, treating or ameliorating medical conditions and  
 PI used as food additives or preservatives.  
 XX  
 PS Claim 11: Page 346; 371pp; English.  
 XX  
 CC The polynucleotide sequences given in AAC79740 to AAC79789 encode the  
 CC human secreted proteins given in AAH44695 to AAH44744. AAH44745 to  
 CC AAH44760 represent human secreted polypeptide sequences and proteins  
 CC homologous to them, which are given in the exemplification of the present  
 CC invention. Human secreted proteins have activities based on the tissues  
 CC and cells the genes are expressed in. Examples of activities include:  
 CC antiarthritic; immunosuppressive; antirheumatic; antiproliferative;  
 CC cytostatic; cardiant; vasodilator; neuro-protective; anti-allergic;  
 CC cerebroprotective; antibacterial; virucide; fungicide; ophthalmological;  
 CC and viderary. The polypeptides and polypeptides can be used to  
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used  
 CC in diagnosing a pathological condition or susceptibility to a  
 CC pathological condition. Disorders which are diagnosed or treated include  
 CC autoimmune diseases, hyperproliferative disorders, cardiovascular  
 CC disorders, cerebrovascular disorders, angiogenesis, nervous system  
 CC disorders, infections caused by bacteria, viruses and fungi and organ  
 CC disorders. The polypeptides can also be used to aid wound healing and  
 CC epithelial cell proliferation, to prevent skin aging due to sunburn, to  
 CC maintain organs before transplantation, for supporting cell culture of  
 CC primary tissues, to regenerate tissues and in chemotaxis. The  
 CC polypeptides can also be used as a food additive or preservative to  
 CC increase or decrease storage capabilities, fat content, lipid, protein,  
 CC carbohydrate, vitamins, minerals, cofactors and other nutritional  
 CC components. AAH73741 to AAH73743 and AAH44744 represent sequences used in  
 CC the exemplification of the present invention.  
 CC  
 XX Sequence 2 AA:  
 SQ  
 Query Match 0.0%; Score 0; DB 21; Length 2;  
 Best local similarity 0.0%; Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0.  
 QY 1 X 1  
 Db 1 m 1  
 DE Human secreted protein sequence encoded by gene 15 SEQ ID NO:75.  
 XX  
 XX Human secreted protein; diagnosis; anti-allergic; immunosuppressive;  
 KM anti-inflammatory; antiproliferative; cytostatic; cardiant; vasotropic;  
 KM cerebroprotective; nociceptive; neuroprotective; antibacterially; virucide;  
 KM fungicide; ophthalmological; viderary; gene therapy; autoimmune disease;

DT 12-FEB-2001 (first entry)  
 XX Human secreted protein encoded by gene 9.  
 DE  
 XX  
 KW Secreted protein; human; immunosuppressive; antiarthritic; antirheumatic;  
 KW antiproliferative; cytosolic; cardiant; vasotropic; cerebroprotective;  
 KW neurotropic; neuroprotective; antibacterial; virucide; fungicide;  
 KW ophthalmological; gene therapy; treatment; autoimmune disease; infection;  
 KW cardiovascular disorder; nervous system disorder; ocular disorder;  
 KW wound healing; epithelial cell proliferation; skin aging; mental state;  
 KW transplantation; metabolism modulation.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 PN W0200055200-A1.  
 XX  
 XX 21-SEP-2000.  
 DE  
 XX 09-MAR-2000; 2000MC-0506042.  
 XX  
 XX 12-MAR-1999; 990S-0124143.  
 PR 03-DEC-1999; 990S-0168663.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Ruben SM, Komatsoulis G;  
 P1  
 P1 WPI: 2000-656008/63.  
 DE N-PSDB: AAC79906.  
 XX  
 XX  
 PT Isolated human secretory proteins, nucleic acids encoding them and  
 PT antibodies directed against them, useful for diagnosing and treating  
 PT disorders related to the proteins such as cancer, Alzheimer's disease  
 PT and Parkinsons -  
 XX  
 XX Claim 11: Page 483; 453pp; English.  
 PS  
 XX This invention describes a novel isolated polypeptide (I) and its  
 CC encoding nucleic acid molecule (II) which have immunosuppressive,  
 CC antirheumatic, antirheumatic, antiproliferative, cytosolic, cardiant,  
 CC vasotropic, cerebroprotective, neurotropic, neuroprotective, antibacterial,  
 CC virucide, fungicide and ophthalmological activity and which can be used  
 CC for gene therapy. (I) and (II) are used to prevent, treat or ameliorate  
 CC a medical condition in e.g. humans, mice, rabbits, goats, horses, cats,  
 CC dogs, chickens or sheep. (I) and (II) are also used in diagnosing a  
 CC pathological condition or susceptibility to a pathological condition. The  
 CC antibodies to (I) can also be used in alleviating symptoms associated  
 CC with the disorders and in diagnostic immunoassays e.g. radioimmunoassays  
 CC or enzyme linked immunosorbent assays (ELISA). Disorders which are  
 CC diagnosed or treated include autoimmune diseases e.g. rheumatoid  
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or  
 CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular  
 CC disorders e.g. cerebral ischemia, angiodystosis, nervous system disorders  
 CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and  
 CC fungi and ocular disorders e.g. corneal infection. The polypeptides can  
 CC also be used to aid wound healing and epithelial cell proliferation. To  
 CC prevent skin aging due to sunburn, to maintain organs before  
 CC transplantation, for supporting cell culture of primary tissues, to  
 CC regenerate tissues and in chemotaxis. The polypeptides are used to  
 CC modulate mammalian metabolism, to change mammal's mental state or  
 CC physical state by influencing biohythms circadian rhythms, depression  
 CC tendency for violence, tolerance for pain, reproductive capabilities,  
 CC hormonal or endocrine levels, appetite, libido, memory, stress or other  
 CC cognitive qualities, as a food additive or preservative, such as to  
 CC increase or decrease storage capabilities, fat content, lipid profile,  
 CC carbohydrates, vitamins, minerals, cofactors or other nutritional  
 CC components.  
 XX  
 XX Sequence 2 AA;  
 SU  
 Query Match 0 0% Score 0 PR 21 Length 2  
 Best Local Similarity 0 0% Pseq No 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 X 1  
 DB 1 1 1  
 RESULT 11  
 ID AAB44951 standard; Protein; 2 AA.  
 AC AAB44951;  
 XX  
 XX AAB44951;  
 DE  
 DT 12-FEB-2001 (first entry)  
 XX  
 XX Human secreted protein encoded by gene 35.  
 DE  
 XX  
 KW Secreted protein; human; immunosuppressive; antiarthritic; antirheumatic;  
 KW antiproliferative; cytosolic; cardiant; vasotropic; cerebroprotective;  
 KW neurotropic; neuroprotective; antibacterial; virucide; fungicide;  
 KW ophthalmological; gene therapy; treatment; autoimmune disease; infection;  
 KW cardiovascular disorder; nervous system disorder; ocular disorder;  
 KW wound healing; epithelial cell proliferation; skin aging; mental state;  
 KW transplantation; metabolism modulation.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 PN W0200055200-A1.  
 XX  
 XX 21-SEP-2000.  
 DE  
 XX 09-MAR-2000; 2000MC-0506042.  
 XX  
 XX 12-MAR-1999; 990S-0124143.  
 PR 03-DEC-1999; 990S-0168663.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Ruben SM, Komatsoulis G;  
 P1  
 P1 WPI: 2000-656008/63.  
 DE N-PSDB: AAC79932.  
 XX  
 XX  
 PT Isolated human secretory proteins, nucleic acids encoding them and  
 PT antibodies directed against them, useful for diagnosing and treating  
 PT disorders related to the proteins such as cancer, Alzheimer's disease  
 PT and Parkinsons -  
 XX  
 XX Claim 11: Page 483; 453pp; English.  
 PS  
 XX This invention describes a novel isolated polypeptide (I) and its  
 CC encoding nucleic acid molecule (II) which have immunosuppressive,  
 CC antirheumatic, antirheumatic, antiproliferative, cytosolic, cardiant,  
 CC vasotropic, cerebroprotective, neurotropic, neuroprotective, antibacterial,  
 CC virucide, fungicide and ophthalmological activity and which can be used  
 CC for gene therapy. (I) and (II) are used to prevent, treat or ameliorate  
 CC a medical condition in e.g. humans, mice, rabbits, goats, horses, cats,  
 CC dogs, chickens or sheep. (I) and (II) are also used in diagnosing a  
 CC pathological condition or susceptibility to a pathological condition. The  
 CC antibodies to (I) can also be used in alleviating symptoms associated  
 CC with the disorders and in diagnostic immunoassays e.g. radioimmunoassays  
 CC or enzyme linked immunosorbent assays (ELISA). Disorders which are  
 CC diagnosed or treated include autoimmune diseases e.g. rheumatoid  
 CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or  
 CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular  
 CC disorders e.g. cerebral ischemia, angiodystosis, nervous system disorders  
 CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and  
 CC fungi and ocular disorders e.g. corneal infection. The polypeptides can  
 CC also be used to aid wound healing and epithelial cell proliferation. To  
 CC prevent skin aging due to sunburn, to maintain organs before  
 CC transplantation, for supporting cell culture of primary tissues, to  
 CC regenerate tissues and in chemotaxis. The polypeptides are used to  
 CC modulate mammalian metabolism, to change mammal's mental state or

CC physical state by interacting hydrophobic interactions, depression  
CC tendency for vitelline follicles, for pain, reproductive capabilities,  
CC hormonal or endocrine levels, appetite, libido, memory, stress or other  
CC cognitive qualities, as a food additive or preservative, such as to  
CC increase or decrease storage capabilities, fat content, lipid, protein,  
CC carbohydrates, vitamins, minerals, cofactors or other nutritional  
CC components.

XX Sequence 2 AA.

Query Match 0.0%; Score 0; DB 21; Length 2;  
Best local Similarity 0.0%; Pct. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1  
DB 1 1 1

#### RESULT 12

AA027796 AAB27796 standard; Protein; 2 AA.

XX AAB27796;

XX 29-JAN-2001 (first entry)

XX Human secreted protein #3.

XX Cytostatic; immunosuppressive; neotropic; neuroprotective; antiviral;  
XX antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;  
XX valvular; anticonvulsant; antibacterial; antifungal; antiparasitic;  
XX cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;  
XX neurological disease; infection; human; secreted protein.

XX Homo sapiens.

XX W020005199-A1.

XX 21-SEP-2000

XX 09-MAR-2000; 2000W0-0806014

XX 12-MAR-1999; 99US-0124095

XX 11-JUN-1999; 99US-0138598

XX 03-DEC-1999; 99US-0168665

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis G;

XX WPI: 2000-572359/53.

XX N-PSDB; AAC59217.

XX Isolated nucleic acid molecule encoding a human secreted protein is

XX used in preventing, treating or ameliorating a medical condition

XX Claim 11; Page 371-372, 433pp, English.

XX Sequences AAB27794-827840 represent the amino acid sequences of 47

XX human secreted proteins encoded by the genes AAC59215-059261. The genes

XX and proteins are useful for preventing, ameliorating or treating medical

XX conditions, e.g. by protein or gene therapy. The genes are isolated from

XX a range of human tissues disclosed in the specification. The nucleic

XX acids, proteins, antibodies and (ant)agonists are useful in the

XX diagnosis, treatment and prevention of: (a) cancer, e.g. breast and

XX ovarian cancer, and other cancers of the adrenal gland, bone, bone

XX marrow, breast, gastrointestinal tract, liver, lung, or urogenital;

XX (b) immune disorders e.g. Addison's disease, allergies, autoimmune

XX hemolytic anemia, autoimmune thyroiditis, diabetes mellitus,

XX Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative

XX colitis; and (c) cardiovascular disorders such as myocardial ischemias;

XX (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and

XX epilepsy; and (f) infectious diseases such as viral, bacterial, fungal

XX and parasitic infections.

XX Sequence 2 AA;

Query Match 0.0%; Score 0; DB 21; Length 2;  
Best local Similarity 0.0%; Pct. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1  
DB 1 1 1

#### RESULT 13

AA027827 AAB27827 standard; Protein; 2 AA.

XX AAB27827;

XX 29-JAN-2001 (first entry)

XX Human secreted protein #34.

XX Cytostatic; immunosuppressive; neotropic; neuroprotective; antiviral;  
XX antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;  
XX valvular; anticonvulsant; antibacterial; antifungal; antiparasitic;  
XX cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;  
XX neurological disease; infection; human; secreted protein.

XX Homo sapiens.

XX W020005199-A1.

XX 21-SEP-2000.

XX 09-MAR-2000; 2000W0-0806014.

XX 12-MAR-1999; 99US-0124095.

XX 11-JUN-1999; 99US-0138598.

XX 03-DEC-1999; 99US-0168665.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis G;

XX WPI: 2000-572359/53.

XX N-PSDB; AAC59248.

XX Isolated nucleic acid molecule encoding a human secreted protein is

XX used in preventing, treating or ameliorating a medical condition

XX Claim 11; Page 385; 433pp; English.

XX Sequences AAB27794-827840 represent the amino acid sequences of 47

XX human secreted proteins encoded by the genes AAC59215-059261. The genes

XX and proteins are useful for preventing, ameliorating or treating medical

XX conditions, e.g. by protein or gene therapy. The genes are isolated from

XX a range of human tissues disclosed in the specification. The nucleic

XX acids, proteins, antibodies and (ant)agonists are useful in the

XX diagnosis, treatment and prevention of: (a) cancer, e.g. breast and

XX ovarian cancer, and other cancers of the adrenal gland, bone, bone

XX marrow, breast, gastrointestinal tract, liver, lung, or urogenital;

XX (b) immune disorders e.g. Addison's disease, allergies, autoimmune

XX hemolytic anemia, autoimmune thyroiditis, diabetes mellitus,

XX Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative

XX colitis; (c) cardiovascular disorders such as myocardial ischemias;

XX (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and

XX epilepsy; and (f) infectious diseases such as viral, bacterial, fungal

XX and parasitic infections.

Sequence 2 AA:

Query Match 0.0%; Score 0; DB 21; Length 2;  
 Host Local Similarity 0.0%; Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
 DB 1 1 1

RESULT 14  
 AAB27830  
 ID AAB27830 standard; Protein: 2 AA.

AC AAB27830;  
 DE 29-JAN-2001 (first entry)  
 XX Human secreted protein #37.  
 XX  
 XX Cytostatic; immunosuppressive; neurotropic; neuroprotective; antiviral;  
 KM antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;  
 KM valvular; anticoagulant; antibacterial; antitubercular; antiparasitic;  
 KM cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;  
 KM neurological disease; infection; human; secreted protein.

XX Homo sapiens.  
 XX  
 XX W0200055199-A1

XX 21-SEP-2000

XX 09-MAR-2000; 2000W0-0506014

XX 12-MAR-1999; 9905-0124095.

XX 11-JUN-1999; 9905-0138598.

XX 01-DEC-1999; 9905-0168665.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis G;

XX WPI: 2000-572359/53.

XX N-PSDB: AAC59251.

XX Claim 11; Page 386; 433pp; English.

XX Sequences AAB27794-B27840 represent the amino acid sequences of 47  
 human secreted proteins encoded by the genes AAC59215-C59261. The genes  
 and proteins are useful for preventing, ameliorating or treating medical  
 conditions, e.g. by protein or gene therapy. The genes are isolated from  
 a range of human tissues disclosed in the specification. The nucleic  
 acids, proteins, antibodies and (ant)agonists are useful in the  
 diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
 ovarian cancer, and other cancers of the adrenal gland, bone, bone  
 marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
 (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
 hemolytic anemia, autoimmune thyroiditis, diabetes mellitus,  
 Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
 colitis; (c) cardiovascular disorders such as myocardial ischemias;  
 (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
 epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
 and parasitic infections.

XX Sequence 2 AA;

Query Match 0.0%; Score 0; DB 21; Length 2;

Host Local Similarity 0.0%; Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
 DB 1 1 1

RESULT 15  
 AAB27834  
 ID AAB27834 standard; Protein: 2 AA.

AC AAB27834;  
 DE 29-JAN-2001 (first entry)  
 XX Human secreted protein #41.

XX Cytostatic; immunosuppressive; neurotropic; neuroprotective; antiviral;  
 KM antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;  
 KM valvular; anticoagulant; antibacterial; antitubercular; antiparasitic;  
 KM cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;  
 KM neurological disease; infection; human; secreted protein.

XX Homo sapiens.  
 XX  
 XX W0200055199-A1.

XX 21-SEP-2000.

XX 09-MAR-2000; 2000W0-0506014

XX 12-MAR-1999; 9905-0124095.

XX 11-JUN-1999; 9905-0138598.

XX 01-DEC-1999; 9905-0168665.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis G;

XX WPI: 2000-572359/53.

XX N-PSDB: AAC59255.

XX Claim 11; Page 387; 433pp; English.

XX Sequences AAB27794-B27840 represent the amino acid sequences of 47  
 human secreted proteins encoded by the genes AAC59215-C59261. The genes  
 and proteins are useful for preventing, ameliorating or treating medical  
 conditions, e.g. by protein or gene therapy. The genes are isolated from  
 a range of human tissues disclosed in the specification. The nucleic  
 acids, proteins, antibodies and (ant)agonists are useful in the  
 diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
 ovarian cancer, and other cancers of the adrenal gland, bone, bone  
 marrow, breast, gastrointestinal tract, liver, lung, or urogenital;  
 (b) immune disorders e.g. Addison's disease, allergies, autoimmune  
 hemolytic anemia, autoimmune thyroiditis, diabetes mellitus,  
 Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
 colitis; (c) cardiovascular disorders such as myocardial ischemias;  
 (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and  
 epilepsy; and (f) infectious diseases such as viral, bacterial, fungal  
 and parasitic infections.

XX Sequence 2 AA;

Query Match 0.0%; Score 0; DB 21; Length 2;  
 Best Local Similarity 0.0%; Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1



Doc 1 m 1

Search completed: September 30, 2001, 10:31:24  
Job time: 154 sec

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OM protein - protein search, using sw model

Run on: September 30, 2001, 10:30:07 : Search time 21.46 Seconds

(without alignments)  
14,265 Million cell updates/sec

File: us-09-498-556-85

Perfect score: 4

Sequence: 1 XXXX 4

Scoring table: RUSUM62

Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: p1r1:  
2: p1r2:  
3: p1r3:  
4: p1r4:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

#### SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	0	0.0	3 2 RHDTTO	thyroloberin - Bom
2	0	0.0	3 2 RHDTT	thyroloberin - pig
3	0	0.0	3 2 RHSHH	thyroloberin - she
4	0	0.0	3 2 A92971	thyroloberin - eas
5	0	0.0	3 2 GKHD	growth-modulating
6	0	0.0	3 2 A60898	bursin - chicken
7	0	0.0	3 2 A23751	spinal cord peptid
8	0	0.0	3 2 B23751	spinal cord peptid
9	0	0.0	3 2 A33852	thyroloberin releas
10	0	0.0	3 2 A2566	thyroloberin releas
11	0	0.0	3 2 P00010	thyroloberin releas
12	0	0.0	3 2 S1864	thyroloberin releas
13	0	0.0	3 2 A43391	thyroloberin releas
14	0	0.0	3 2 E37196	thyroloberin releas
15	0	0.0	3 2 F27196	thyroloberin releas
16	0	0.0	3 2 F27196	thyroloberin releas
17	0	0.0	3 2 F27196	thyroloberin releas
18	0	0.0	3 2 F27196	thyroloberin releas
19	0	0.0	3 2 F27196	thyroloberin releas
20	0	0.0	3 2 F27196	thyroloberin releas
21	0	0.0	3 2 F27196	thyroloberin releas
22	0	0.0	3 2 F27196	thyroloberin releas
23	0	0.0	3 2 F27196	thyroloberin releas
24	0	0.0	3 2 F27196	thyroloberin releas
25	0	0.0	3 2 F27196	thyroloberin releas
26	0	0.0	3 2 F27196	thyroloberin releas
27	0	0.0	3 2 F27196	thyroloberin releas
28	0	0.0	3 2 F27196	thyroloberin releas
29	0	0.0	3 2 F27196	thyroloberin releas

30	0	0.0	4 2 PL0146	carbon-monoxide de
31	0	0.0	4 2 A37832	phenol 2-methoxyge
32	0	0.0	4 2 A48360	gamma subunit of p
33	0	0.0	4 2 A40697	biotin A - Citoba
34	0	0.0	4 2 A61300	22K superhelical D
35	0	0.0	4 2 157745	D-mannanase hydrol
36	0	0.0	4 2 A41890	protein D - Escher
37	0	0.0	4 2 D43014	hypothetical prote
38	0	0.0	4 2 D41654	hypothetical prote
39	0	0.0	4 2 B43848	cell surface adhes
40	0	0.0	4 2 140505	hypothetical prote
41	0	0.0	4 2 140870	phospholipase C (E
42	0	0.0	4 2 140804	endothucanase P -
43	0	0.0	4 2 T46627	hypothetical prote
44	0	0.0	4 2 S09478	globulin IV alpha
45	0	0.0	4 2 S53508	starvation induced

#### ALIGNMENTS

RESULT 1  
RHDTTO  
thyroloberin - Bombina orientalis  
C:Species: Bombina orientalis  
C:Date: 31-Dec-1993 \*seqproc\_revision 12-May-1995 \*text\_change 20-Mar-1998  
C:Accession: A90919; A01415  
R:Yasuhara, T.; Nakajima, T.  
Chem. Pharm. Bull. 23, 3301-3303, 1975  
A:Title: Occurrence of thyrolobin-Pro-NH-2 in the frog skin.  
A:Reference number: A90919; M01D:76138399  
A:Accession: A90919  
A:Molecule type: protein  
A:Residues: 1-3 (YAS)  
C:Superfamily: thyrolobin precursor  
C:Keywords: amidated carboxyl end, catenones (acid), hormone; pyroglutamic acid  
F1/Modified site: pyroglutamate carboxylic acid (Glu) \*status experimental  
F3/Modified site: amidated carboxyl end (Pro) \*status experimental

Query Match Similarity 0.0%; Score 0; DB 2; Length 3;  
Best local 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
DB 1 Q 1

RESULT 2  
RHDTT  
thyroloberin - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 23-Oct-1991 \*seqproc\_revision 12-May-1995 \*text\_change 20-Mar-1998  
C:Accession: A01415  
R:Ritt, P.W.G.; Barrett, J.F.; Roberts, C.V.; Shelly, A.V.  
Biochem. J. 269, 1103-1106, 1990  
A:Title: Structure of porcine thyrolobin releasing hormone.  
A:Reference number: A90565; M01D:76136150  
A:Accession: A01415  
A:Molecule type: protein  
A:Residues: 1-3 (SHL)  
F:Ritt, P.W.G.; Barrett, J.F.; Roberts, C.V.; Shelly, A.V.  
Biochem. J. 269, 1103-1106, 1990  
A:Title: The identity of chemical and hormonal precursors of the thyrolobin P-1-Asn  
A:Reference number: A90567; M01D:7003904  
A:Contents: annotation  
A:Notes: thyrolobin and thyrolobin and of values (in 12 chromatographic systems) of the sy  
C:Superfamily: thyrolobin precursor  
C:Keywords: amidated carboxyl end, hormone; pyroglutamic acid  
F1/Modified site: pyroglutamate carboxylic acid (Glu) \*status experimental  
F3/Modified site: amidated carboxyl end (Pro) \*status experimental

Query Match 0.0% Score 0; DB 2; Length 3;  
 Best Local Similarity 0.0% Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

UY 1 X 1  
 DB 1 G 1

#### RESULT 4

Species: sheep

Species: ovis orientalis aries, ovis ammon aries (domestic sheep)

CiDate: 31-Dec-1991 #sequence\_revision: 12 Mar, 1995 #text\_change: 20 Mar, 1996

CiAccession: A94750; A01415

CiAuthor: J.R., D.M.; Burgess, R.; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.

CiTitle: The elucidation of the primary structure of the hypothalamic thyrotrophic stimulating

CiReference number: A94750

A:Accession: A94750

A:Molecule type: protein

A:Residues: 1-4 <HS>

A:Note: R.; Dunn, T.F.; Desiderio, D.; Ward, D.N.; Vale, W.; Guillemin, R.

A:Title: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.

A:Reference number: A94161; M01D:7016386

A:Contents: annotation

A:Note: physicochemical characteristics and biological activities of the natural and syn-

CiKeywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F3/Modified site: pyroglutamic carboxyl end (Pro) #status experimental

Query Match 0.0% Score 0; DB 2; Length 3;  
 Best Local Similarity 0.0% Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

UY 1 X 1  
 DB 1 G 1

#### RESULT 4

Species: eastern newt (tentative sequence)

Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)

CiDate: 31-Dec-1991 #sequence\_revision: 31-Dec-1991 #text\_change: 20-Mar-1996

CiAccession: A92971; A01415

CiAuthor: J.R.; Burgess, R.; Dunn, T.F.

CiTitle: Biosynthesis of thyrotrophic releasing factor by newt (Triturus viridescens) bta

A:Accession: A92971; M01D:75035605

A:Molecule type: protein

A:Residues: 1-3 <HS>

A:Note: a peptide with the chromatographic and electrophoretic characteristics of thyro-

CiKeywords: amidated carboxyl end; glutamic acid; hormone; hypothalamus; pyroglutamic

F3/Modified site: pyroglutamic carboxyl end (Pro) #status experimental

Query Match 0.0% Score 0; DB 2; Length 3;  
 Best Local Similarity 0.0% Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

UY 1 X 1  
 DB 1 G 1

#### RESULT 5

Species: human

Species: Homo sapiens (man)

CiDate: 22-Oct-1981 #sequence\_revision: 24 May 1995 #text\_change: 20 Jun 2000

CiAccession: A01421

CiAuthor: R.; Schlesselman, D.H.; Pickart, L.; Thaler, M.M.

CiTitle: Growth-modulating serum tripeptide is glyxyl-histidyl-lysine.

A:Reference number: A01421; M01D:77162369

A:Accession: A01421

A:Molecule type: protein

A:Residues: 1-3 <SCM>

A:Note: this serum tripeptide is found to stimulate growth of some cell types and to

Query Match 0.0% Score 0; DB 2; Length 3;  
 Best Local Similarity 0.0% Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

UY 1 X 1  
 DB 1 G 1

#### RESULT 6

Species: chicken

Species: Gallus gallus (chicken)

CiDate: 31-Dec-1993 #sequence\_revision: 31-Dec-1993 #text\_change: 18 Aug 2000

CiAccession: A60898

CiAuthor: R.; Kroon, D.; Heavner, G.; Viamonte, G.; Goldstein, G.

CiTitle: Tripeptide structure of bursin, a selective B-cell-differentiating hormone o

A:Reference number: A60898; M01D:86122916

A:Accession: A60898

A:Molecule type: protein

A:Residues: 1-3 <AUD>

A:Superfamily: unassigned animal peptides

CiKeywords: amidated carboxyl end; hormone

F3/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 0.0% Score 0; DB 2; Length 3;  
 Best Local Similarity 0.0% Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

UY 1 X 1  
 DB 1 K 1

#### RESULT 7

Species: pig

Species: Sus scrofa domestica (domestic pig)

CiDate: 28-Sep-1987 #sequence\_revision: 28-Sep-1987 #text\_change: 18-Aug-2000

CiAccession: A23751

CiAuthor: R.; Hsi, K.; Chou, R.L.; Chou, C.C.; Chang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou

CiTitle: Biochem. Biophys. 240, 178-184, 1985

A:Reference number: A23751; M01D:85250425

A:Accession: A23751

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-3 <HS1>

C:Superfamily: unassigned animal peptides

Query Match 0.0% Score 0; DB 2; Length 3;  
 Best Local Similarity 0.0% Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1  
DB 1 Q 1

RESULT 8

R23751

spinal cord peptide SCP-5 - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 28-Sep-1987 #sequence\_revision 28 Sep 1987 #text\_change 18 Aug 2000

C:Accession: R23751

R:Hist, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K.

Arch. Biochem. Biophys. 240:178-183, 1985

A:Reference number: A23751

A:Accession: R23751

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-3-4835

C:Superfamily: unassigned animal peptides

Query Match 0.0% Score 0; DB 2; Length 3;  
Best local similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1

DB 1 M 1

RESULT 9

A33802

thyrotropin-releasing hormone-like peptide - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 27-Feb-1990 #sequence\_revision 31-Dec-1992 #text\_change 18-Aug-2000

C:Accession: A33802

R:Cockle, S.M.; Aitken, A.; Bay, F.; Smyth, D.G.

J. Biol. Chem. 264:7798-7799, 1989

A:Title: A novel peptide, pyroglutamylglutaminylproline amide, in the rabbit prostate comp

A:Reference number: A33802

A:Accession: A33802

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-3-6005

C:Superfamily: unassigned animal peptides

C:Keywords: inhibitor; antioxy; and; pyroglutamic acid

E1/Modified site: pyroglutamic acid (Gln) #status experimental

E3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0% Score 0; DB 2; Length 3;  
Best local similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1

DB 1 Q 1

RESULT 10

A22565

R-phycoerythrin alpha-1 chain - red alga (Gastrocoulonum coulteri) (fragment)

C:Species: Gastrocoulonum coulteri

C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993

C:Accession: A22565

R:Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260:4856-4863, 1985

A:Title: Characterization of the bilin attachment sites on R-phycoerythrin

A:Reference number: A22565

A:Accession: A22565

A:Molecule type: protein

A:Keywords: 1 X 1

Query Match 0.0% Score 0; DB 2; Length 3;  
Best local similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1

DB 1 Q 1

RESULT 11

P00010

angiotensin converting enzyme inhibitor (FIP-3) common fig

R:Alvarado-Lam, L.; Irujo-Larrea, I.

C:Species: Ficus carica (common fig)

C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 08-Dec-1995

C:Accession: P00010

R:Maruyama, S.; Miyoshi, S.; Tanaka, H.

Agric. Biol. Chem. 52:2763-2767, 1989

A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.

A:Reference number: P00008

A:Accession: P00010

A:Molecule type: protein

A:Residues: 1-3-4835

A:Experimental source: latex

C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 0.0% Score 0; DB 2; Length 3;  
Best local similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1

DB 1 L 1

RESULT 12

S13894

histidinol dehydrogenase (EC 1.1.1.22) wild cabbage (fragment)

C:Species: Brassica oleracea (wild cabbage)

C:Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 06-Jun-1997

C:Accession: S13894

R:Nadal, A.; Scheidegger, A.

Arch. Biochem. Biophys. 280:127-132, 1991

A:Title: Purification and characterization of histidinol dehydrogenase from cabbage.

A:Reference number: S13894

A:Accession: S13894

A:Molecule type: protein

A:Residues: 1-3-5805

A:Experimental source: var capitata

C:Keywords: dimer; NAD; oxidoreductase

Query Match 0.0% Score 0; DB 2; Length 3;  
Best local similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 X 1

DB 1 X 1

RESULT 13

A43391

TRH-like tripeptide - alfalfa

C:Species: Medicago sativa (alfalfa)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C:Accession: A43391

R:Lackey, D.B.

J. Biol. Chem. 267:17508-17511, 1992

A:Title: Isolation and structural determination of a novel TRH-like tripeptide from

A:Reference number: A43391; MUID:92388092

A:Accession: A4391

A:Molecule type: protein

A:Residues: 1-3 <1AC>

C:Keywords: amidated carboxyl end; pyrrolutamic acid

F1/Modified site: pyrrolidone carboxylic acid (Gln) \*status experimental

F1/Modified site: amidated carboxyl end (Pro) \*status experimental

#### Query Match

Best Local Similarity 0.0%; Score 0; DB 2; Length 3;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

DB 1 Q 1

#### RESULT 14

E47196

bradykinin-potentiating peptide 5 - island jararaca

C:Species: Bothrops jararalis (island jararaca)

C>Date: 14-Feb-1992 \*sequence\_revision 01-Dec-1992 \*text\_change 05-Aug-1994

C:Accession: E47196

R:Pintra, A.C.O.; Vieira, C.A.; Gagliolo, J.R.

J. Protein Chem. 9, 221-227, 1990

A:Title: Primary structure and biological activity of bradykinin potentiating peptides

A:Reference number: A47196; MUID:90351557

A:Accession: E47196

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-3 <CIN>

C:Keywords: pyrrolutamic acid

F1/Modified site: pyrrolidone carboxylic acid (Gln) \*status experimental

#### Query Match

Best Local Similarity 0.0%; Score 0; DB 2; Length 3;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

DB 1 Q 1

#### RESULT 15

E47196

bradykinin-potentiating peptide 6 - island jararaca

C:Species: Bothrops jararalis (island jararaca)

C>Date: 14-Feb-1992 \*sequence\_revision 01-Dec-1992 \*text\_change 05-Aug-1994

C:Accession: E47196

R:Pintra, A.C.O.; Vieira, C.A.; Gagliolo, J.R.

J. Protein Chem. 9, 221-227, 1990

A:Title: Primary structure and biological activity of bradykinin potentiating peptides

A:Reference number: A47196; MUID:90351557

A:Accession: E47196

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-3 <CIN>

C:Keywords: pyrrolutamic acid

F1/Modified site: pyrrolidone carboxylic acid (Gln) \*status experimental

#### Query Match

Best Local Similarity 0.0%; Score 0; DB 2; Length 3;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

DB 1 Q 1







GenCore version 4.5  
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OM protein - protein search, using SW model

Run on: September 30, 2001, 10:29:34 Search time: 13.87 seconds  
(without alignments)  
9.879 Million cell updates/sec

Title: US-09-498-556-85

Perfect score: 4  
Sequence: 1 XXXX 4

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 93435 seqs, 44255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_39\*

pred No is the number of results predicted by change to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	0	0.0	3	1 GRWM_HUMAN	P01157 homo sapien
2	0	0.0	3	1 TMF_VIBRI	P24272 vibrio fisch
3	0	0.0	3	1 TMF_PIG	P01151 sus scrofa
4	0	0.0	4	1 ACHL_ACHER	P35244 acharia fa
5	0	0.0	4	1 DCM_L_PSECH	P13916 pseudomonas
6	0	0.0	4	1 DCM_L_PSECH	P13918 pseudomonas
7	0	0.0	4	1 EOSTI_HUMAN	P02731 homo sapien
8	0	0.0	4	1 PAP3_HTFME	P42562 hitudo medi
9	0	0.0	4	1 PAP3_HTFME	P42563 hitudo medi
10	0	0.0	4	1 FLPE_HTFME	P42561 hitudo medi
11	0	0.0	4	1 FMRE_MAVNI	P01162 macrocallis
12	0	0.0	4	1 PMO1_YEAST	P36515 saccharomyc
13	0	0.0	4	1 TMF_HUMAN	P01858 homo sapien
14	0	0.0	5	1 ALI4_CARMA	P81817 carcinus ma
15	0	0.0	5	1 RHOA_CITTF	P13071 citrobacter
16	0	0.0	5	1 RHOA_CITTF	P12677 salmonella
17	0	0.0	5	1 RHOA_CITTF	P12677 salmonella
18	0	0.0	5	1 RHOA_CITTF	P12677 salmonella
19	0	0.0	5	1 BPP7_BOVIN	P30425 bolitropis in
20	0	0.0	5	1 FARP_AKTR	P41853 ateloposth
21	0	0.0	5	1 FARP_PARMA	P81864 pardachinus
22	0	0.0	5	1 PRGT_PERAM	P01373 periplaneta
23	0	0.0	5	1 SINGA_ACTHO	P19991 acthea dome
24	0	0.0	5	1 TPIS_CANEA	P54714 canis famli
25	0	0.0	5	1 TRM3_BECUL	P13973 escherichia
26	0	0.0	5	1 TMF2_MAVIF	P36528 sus scrofa (m
27	0	0.0	5	1 UPH1_MOUSE	P34634 mus musculu
28	0	0.0	5	1 UH44_CHITS	P34634 mus musculu
29	0	0.0	6	1 ACPL_PAPRT	P23736 mytilus edu
30	0	0.0	6	1 CIP1_MYTED	P13737 mytilus edu
31	0	0.0	6	1 CIP2_MYTED	P13737 mytilus edu
32	0	0.0	6	1 FARP_MONIFX	P41966 monilezia ex
33	0	0.0	6	1 LOK1_LOCOMI	P41491 locusta mig

34	0	0.0	6	1 CVM_LEPDE	P42985 leptinotars
35	0	0.0	6	1 TMF_SARBU	P41495 sarcophaga
36	0	0.0	6	1 TMF1_PSHPI	P34414 pseudomonas
37	0	0.0	6	1 UN06_CLOPA	P81351 clostridium
38	0	0.0	6	1 VP19_HSVIK	P23210 herpes simp
39	0	0.0	7	1 ALI2_CARMA	P81805 carcinus ma
40	0	0.0	7	1 ALI3_CARMA	P81806 carcinus ma
41	0	0.0	7	1 ALI4_CARMA	P81807 carcinus ma
42	0	0.0	7	1 ALI5_CARMA	P81808 carcinus ma
43	0	0.0	7	1 ALI7_CYDPO	P82158 cydia pomon
44	0	0.0	7	1 CARP_MYED	P10420 mytilus edu
45	0	0.0	7	1 UN06_PINPS	P81675 pinus pinas

#### ALIGNMENTS

RESULT 1  
GRWM\_HUMAN STANDARD: PRT: 3 AA.  
ID GRWM\_HUMAN  
AC P01157  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last annotation update)  
DE GROWTH-MODULATING PEPTIDE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eularchia; Primates; Catarrhini; Hominoidea; Homo.  
RN [1]  
RP NCB1\_TaxID:9606;  
RX MEDLINE:77162369; Pubmed 858356;  
PA Schlesinger P.H., Probert L., Thaler M.M.:  
"Growth-modulating serum lipopeptide is Glycyl-Histidyl-Lysine";  
KL Experientia 33:324-325(1977).  
CC -I- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE  
CC GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.  
DR PIR: A01421; GKHU.  
SQ SEQUENCE 3 AA: 340 MW: 6331810000000000 GPC64;

Query Match 0.0% Score 0.0 PRT: Length 3;  
Host Local Similarity 0.0% Pred No 0;  
Matches 0 Conservative 0 Mismatches 1 Indels 0 Gaps 0;  
UY 1 X 1  
nb 1 G 1  
RESULT 2  
LUXE\_VIBRI STANDARD: PRT: 3 AA.  
ID LUXE\_VIBRI  
AC P24272;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE LONG-CHAIN-FATTY-ACID-LIPOPEPTIN-COMPONENT LIGASE (EC 6.2.1.19)  
DE (ACYL-PROTEIN SYNTHETASE) (FRAGMENT).  
GN LUXE.  
OS Vibrio fischeri.  
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.  
OX NCBI\_TaxID:668;  
RN [1]  
RP SEQUENCE FROM N.A.  
EX MEDLINE 21972326; Pubmed 2251256;  
PA Swartzman E., Kapoor S., Graham A.F., Melnyk E.A.:  
"A new Vibrio fischeri lux gene encodes a bidirectional termination  
ET site for the lux operon";  
RL J Bacteriol 172:6797-6802(1990).  
CC FUNCTION: ACT. PROTEIN SYNTHETASE ACTIVATES TETRAHYDROIC ACID.  
CC IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE  
CC FOR CONVERTING TETRAHYDROIC ACID TO THE ALDEHYDE WHICH SERVES AS

CC SUBSTRATE IN THE 11 $\alpha$ -HYDROXYLASE-CATALYZED REACTION  
 CC -1- CATALYTIC ACTIVITY: ATP + AN ACID + PROTEIN - AMP + PYROPHOSPHATE  
 CC + AN ACTI-PROTEIN THIOESTER.  
 CC -1- PATHWAY: SECOND STEP IN THE BIOLUMINESCENT FATTY ACID REDUCTASE  
 CC COMPLEX.  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL: M2812; NOT\_ANNOTATED\_CDS.  
 CC Bioluminescence: Lipase.  
 CC F1: 1  
 CC SEQUENCE: 4 AA; 374 MW; 6AA4404000000000 CPO64;  
 CC  
 CC Query Match: 0.0%; Score 0; DB 1; Length 3;  
 CC Best Local Similarity: 0.0%; Prod. No. 0;  
 CC Matches: 0; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;  
 CC  
 CC QY 1 X 1  
 CC Db 1 1 1  
 CC  
 CC RESULT 4  
 CC TRHL\_PIC STANDARD; PRT; 4 AA.  
 CC AC P0151;  
 CC 21-JUN-1986 (Rel. 01, Created)  
 CC 21-JUN-1986 (Rel. 01, Last sequence update)  
 CC 15-DEC-1998 (Rel. 37, Last annotation update)  
 CC TRHOLIBERIN (THYROTROPIN-RELEASING HORMONE) (TRH).  
 CC Sus scrofa (Pig), ovis aries (Sheep),  
 CC Bombina orientalis (Oriental fire-bellied toad), and  
 CC Neotrophalium viridescens (Eastern newt) (Triturus viridescens).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suis.  
 CC NCBI\_TaxID: 9823, 9940, 8346, 8316;  
 CC RN [1]  
 CC SPECIES: Pig; TISSUE: Hypothalamus;  
 CC RX MEDLINE: 7016150; PubMed 4984938;  
 CC Nair R.M.G., Barrett J.F., Howers C.Y., Schally A.V.;  
 CC "Structure of porcine thyrotropin releasing hormone";  
 CC Biochemistry 9:1103-1106(1970).  
 CC RN [2]  
 CC SYNTHESIS:  
 CC SPECIES: Pig;  
 CC RX MEDLINE: 70039904; PubMed 4982117;  
 CC Heller J., Ezemann F., Folkers K., Bowers C.Y., Schally A.V.;  
 CC "The identity of chemical and hormonal properties of the thyrotropin  
 CC releasing hormone and pyroglutamyl-histidyl-proline amide";  
 CC Biochem. Biophys. Res. Commun. 37:705-710(1969).  
 CC RN [3]  
 CC SEQUENCE:  
 CC SPECIES: Sheep; TISSUE: Hypothalamus;  
 CC Desiderio D.M. Jr., Burgess R., Dunn T.F., Vale W., Gullermin R.;  
 CC Ward D.N.;  
 CC "The elucidation of the primary structure of the hypothalamic thyrotid  
 CC stimulating hormone releasing factor of ovine origin by means of mass  
 CC spectrometry";  
 CC J. Biol. Chem. 258:1228(1971).  
 CC RN [4]  
 CC SYNTHESIS:  
 CC SPECIES: Sheep;  
 CC RX MEDLINE: 70163386; PubMed 4985794;  
 CC Burgess R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,  
 CC Gullermin R.;

RT "Characterization of ovine hypothalamic hypophysiotropic  
 RT TRH-releasing factor";  
 RT Nature 225:321-325(1970).  
 RT RN [5]  
 RT SEQUENCE:  
 RT SPECIES: R.orientalis; TISSUE: SKIN;  
 RT RX MEDLINE: 7613839; PubMed-815011;  
 RT Yasuhara T., Nakajima T.;  
 RT "Isolation and characterization of the TRH  
 RT releasing factor from skin";  
 RT J. Neurochem. 23:471-478(1974).  
 RT CC  
 CC -1- FUNCTION: TRH FUNCTIONS AS A REGULATOR OF THE BIOSYNTHESIS OF TRH  
 CC IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/  
 CC NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.  
 CC DE PIR: A01415; RHPGT.  
 CC DR PIR: A93750; RHPGT.  
 CC DR PIR: A93750; RHPGT.  
 CC DR PIR: A92971; A92971.  
 CC KW Annotation.  
 CC FT MOD\_RES 1 1 PYROLYSINE CARBOXYLIC ACID.  
 CC FT MOD\_RES 3 4 AMIDATION.  
 CC SQ SEQUENCE 3 AA; 380 MW; 7761F6H000000000 CPO64;  
 CC  
 CC Query Match: 0.0%; Score 0; DB 1; Length 3;  
 CC Best Local Similarity: 0.0%; Prod. No. 0;  
 CC Matches: 0; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;  
 CC  
 CC QY 1 X 1  
 CC Db 1 0 1  
 CC  
 CC RESULT 4  
 CC ACHL\_ACHPU STANDARD; PRT; 4 AA.  
 CC AC P35904;  
 CC 01-JUN-1994 (Rel. 29, Created)  
 CC 01-JUN-1994 (Rel. 29, Last sequence update)  
 CC 15-JUN-1998 (Rel. 36, Last annotation update)  
 CC ACHALLIN-1.  
 CC US Achatina fulica (Giant African snail).  
 CC OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 CC OC Achatinacea; Achatinidae; Achatina.  
 CC OX NCBI\_TaxID: 6530;  
 CC RN [1]  
 CC SEQUENCE: CHARACTERIZATION, AND SYNTHESIS.  
 CC STRAIN: FERUSSAC; TISSUE: GANGLION;  
 CC RX MEDLINE: 89273551; PubMed-2597281;  
 CC Kametani Y., Minakata H., Kency P.T.M., Iwashita T., Watanabe K.,  
 CC Kametani K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,  
 CC Novales E.T., Kanapi C.G., Takayoshi H., Nemoto K.;  
 CC "Achatin-1, an endogenous neuroexcitatory tetrapeptide from Achatina  
 CC fulica pennsylvanica containing a D-amino acid residue";  
 CC Biochem. Biophys. Res. Commun. 160:1015-1020(1989).  
 CC RN [2]  
 CC CHARACTERIZATION:  
 CC RX MEDLINE: 91264856; PubMed-1675568;  
 CC Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nemoto K.,  
 CC Yoshida M., Harada A., Kaneoka Y., Kobayashi M.;  
 CC "Purification of achatin-1 from the African giant snail,  
 CC Achatina fulica, and its possible function";  
 CC Biochem. Biophys. Res. Commun. 177:847-853(1991).  
 CC RN [3]

```

RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=93014529; PubMed 1399265;
RA Ishida T., In Y., Doi M., Yasuda-Kamatani Y., Minakata H.,
RA Washita T., Nemoto K.;
RT "CRYSTAL STRUCTURE AND MOLECULAR CONFORMATION OF ACETALIN-1
RT (H-D-tyl-D-Phe-Ala-Asp-CH3) ON ENDOGENOUS NEUROPEPTIDE-CONTAINING A
RT D-AMINO ACID RESIDUE."
RL Int. J. Pept. Protein Res. 49:258-264(1992)
CC -FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
CC AND PROGRESSES A SPIKE REMAINING OF THE IDENTIFIED HEART EXCITATORY
CC NEURON (PUN); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
CC HEART BEAT. HAS ALSO AN EFFECT ON SYMPATHIC OTHER MUSCLES.
PR: A32480; A22480.
RW Homomer: D-AMINO acid.
FT MOD_RES 2
FT NON_TER 2
SQ SEQUENCE 4 AA: 408 MW: 66ADDE9C8100000000 GRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 G 1

RESULT 5
ID ICM_PSECH STANDARD; PRT; 4 AA.
AC P19916;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE CARBON MONOXIDE DEHYDROGENASE LARGE CHAIN (EC 1.2.99.2) (FRAGMENT).
OS Pseudomonas carboxydohydrogena
OC Bacteria; Proteobacteria.
GX NCBI_Taxid=290;
KN (1)
RP SEQUENCE.
RX MEDLINE=90055678; PubMed 2818128;
RA Kriat M., Hugendieck L., Herwig S., Meyer O.;
RT "HOMOLOGY AND DISTRIBUTION OF CO DEHYDROGENASE STRUCTURAL GENES IN
RT CARBOXYDOTROPHIC BACTERIA."
RL Arch. Microbiol. 152:335-341(1989)
CC -FUNCTION: CO + H(2)O + ACCEPTOR -> CO(2) + REDUCED
CC ACCEPTOR.
CC -CORFACTOR: MOLYBDENUM.
CC -SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
DR PIR: P10146; P10146
RW Oxidoreductase; Molybdenum.
FT MOD_RES 4
FT NON_TER 4
SQ SEQUENCE 4 AA: 441 MW: 7761P976100000000 GRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 M 1

RESULT 6
ID ICM_PSECH STANDARD; PRT; 4 AA.
AC P19918;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE CARBON MONOXIDE DEHYDROGENASE SMALL CHAIN (EC 1.2.99.2) (FRAGMENT)

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OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria.
GX NCBI_Taxid=290;
KN (1)
RP SEQUENCE.
RX MEDLINE=90055678; PubMed 2818128;
RA Kriat M., Hugendieck L., Herwig S., Meyer O.;
RT "HOMOLOGY AND DISTRIBUTION OF CO DEHYDROGENASE STRUCTURAL GENES IN
RT CARBOXYDOTROPHIC BACTERIA."
RL Arch. Microbiol. 152:335-341(1989)
CC -FUNCTION: CO + H(2)O + ACCEPTOR -> CO(2) + REDUCED
CC ACCEPTOR.
CC -CORFACTOR: MOLYBDENUM.
CC -SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
DR PIR: P10146; P10146.
RW Oxidoreductase; Molybdenum.
FT MOD_RES 4
FT NON_TER 4
SQ SEQUENCE 4 AA: 420 MW: 66333996F000000000 GRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 M 1

RESULT 7
ID EOST_HUMAN STANDARD; PRT; 4 AA.
AC P62731;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE EOSTINOPHILINOTACTIC PEPTIDES.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Eumetazoa;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo
GX NCBI_Taxid=9606;
KN (1)
RP SEQUENCE.
RX MEDLINE=7607412; PubMed 1060093;
RA Goebel E.F., Austen K.F.;
RT "Purification and synthesis of eosinophilotoxic tetrapeptides of
RT human lung tissue: identification as eosinophil chemotactic factor of
RT anaphylaxis."
RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
CC -FUNCTION: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG
CC (AND OTHER TISSUES) PROVING HYPERSENSITIVITY REACTIONS
CC (ANAPHYLAXIS). THEIR ACTIVITIES, PREPREFERENTIALLY AFFECTING
CC EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE
CC OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.
DR PIR: A03190; ETHOL.
FT VARIANT 1 V -> A (IN OTHER PEPTIDE).
FT MOD_RES 1
FT NON_TER 1
SQ SEQUENCE 4 AA: 300 MW: 8B0569B2A000000000 GRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 V 1

RESULT 8
ID FAP4_HIRME STANDARD; PRT; 4 AA.
AC FAP4_HIRME
FT MOD_RES 1
FT NON_TER 1
SQ SEQUENCE 4 AA: 408 MW: 66ADDE9C8100000000 GRC64;

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AC P42562;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide YMRP-AMIDE.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinoidea; Hirudinifformes; Hirudinidae; Hirudo
NCBI_TaxID 6421;
KW SEQUENCE.
RA MEDLINE-92195954; PubMed-166933;
RA Evans B.D., Pohl J., Karlsonis M.A., Calabrese R.L.;
RT "Identification of Rhamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991)
CC -1- SIMILARITY: REFERENCES TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES.
SQ SEQUENCE 4 AA: 598 MW: 6914073830000000 GPG64;

Query Match 0.0%; Score 0; DB 1; Length 4;
Best local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

UY 1 X 1
DB 1 Y 1

RESULT 9
FAR4_HIRME STANDARD: PRT: 4 AA.
ID FAR4_HIRME
AC P42563;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide YMRP-AMIDE.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinoidea; Hirudinifformes; Hirudinidae; Hirudo
NCBI_TaxID 6421;
KW SEQUENCE.
RA MEDLINE-92195954; PubMed-166933;
RA Evans B.D., Pohl J., Karlsonis M.A., Calabrese R.L.;
RT "Identification of Rhamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991)
CC -1- SIMILARITY: REFERENCES TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES.
SQ SEQUENCE 4 AA: 616 MW: 6914068830000000 GPG64;

Query Match 0.0%; Score 0; DB 1; Length 4;
Best local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

UY 1 X 1
DB 1 Y 1

RESULT 10
FIR4_HIRME STANDARD: PRT: 4 AA.
ID FIR4_HIRME
AC P42561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide YMRP-AMIDE.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinoidea; Hirudinifformes; Hirudinidae; Hirudo
NCBI_TaxID 6421;
KW SEQUENCE.
RA MEDLINE-92195954; PubMed-166933;
RA Evans B.D., Pohl J., Karlsonis M.A., Calabrese R.L.;
RT "Identification of Rhamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991)
CC -1- SIMILARITY: REFERENCES TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES.
SQ SEQUENCE 4 AA: 616 MW: 6914068830000000 GPG64;

Query Match 0.0%; Score 0; DB 1; Length 4;
Best local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

UY 1 X 1
DB 1 Y 1

RESULT 11
FMRP_MACNI STANDARD: PRT: 4 AA.
ID FMRP_MACNI
AC P01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-1994 (Rel. 36, Last annotation update)
DE FMRFamide (PEAK C) (CARDIOEXCITATORY NEUROPEPTIDE).
OS Macrocallista nimbosa (Sun-ray clam), Nereis virens (Sandworm),
OS Hirudo medicinalis (Medicinal leech), and Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
OC Veneroidae; Veneridae; Macrocallista.
NCBI_TaxID=6594, 6353, 6421, 27815;
KW SEQUENCE. AND SYNTHESIS.
PP SPECIES-M. nimbosa; TISSUE-Cerebral pedal, and Visceral ganglion;
RC MEDLINE-77215956; PubMed-877582;
RA Price D.A., Greenberg M.T.;
RT "Structure of a molluscan cardioexcitatory neuropeptide.";
RL Science 197:670-671(1977).
RN [12]
PP SPECIES-M. nimbosa; TISSUE-Ganglion;
RC SPECIES-M. nimbosa; TISSUE-Ganglion;
RA MEDLINE-78012038; PubMed-909875;
RA Price D.A., Greenberg M.J.;
RT "Purification and characterization of a cardioexcitatory neuropeptide from the central ganglia of a bivalve mollusc.";
RL Pref. Biochem. 7:261-281(1977)
RN [13]
PP SPECIES-N. virens;
RC SPECIES-N. virens;
RA MEDLINE-90259856; PubMed-2342992;
RA Krahnak K.G., Price D.A.;
RT "Authentic FMRFamide is present in the polychaete Nereis virens.";
RL Peptides 11:75-77(1990).
RN [4]
KW SEQUENCE.
RC SPECIES-H. medicinalis;

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US Hirudo medicinalis (Medicinal leech), and Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinoidea; Hirudinifformes; Hirudinidae; Hirudo.
OC Aynchobdellidae; Hirudinifformes; Hirudinidae; Hirudo.
NCBI_TaxID 6421, 27815;
RN [1]
PP SPECIES-H. medicinalis;
RC SPECIES-H. medicinalis;
RA MEDLINE-92195954; PubMed-166933;
RA Evans B.D., Pohl J., Karlsonis M.A., Calabrese R.L.;
RT "Identification of Rhamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
RN [2]
PP SPECIES-H. trivolvis; TISSUE-Kidney;
RC SPECIES-H. trivolvis; TISSUE-Kidney;
RA MEDLINE-94286417; PubMed-7912428;
RA Madrid K.P., Price D.A., Greenberg M.T., Khan H.P., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma trivolvis.";
RL Peptides 15:31-36(1994).
CC -1- SIMILARITY: REFERENCES TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES.
SQ SEQUENCE 4 AA: 592 MW: 69097290000000 GPG64;

Query Match 0.0%; Score 0; DB 1; Length 4;
Best local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

UY 1 X 1
DB 1 F 1

RESULT 11
FMRP_MACNI STANDARD: PRT: 4 AA.
ID FMRP_MACNI
AC P01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-1994 (Rel. 36, Last annotation update)
DE FMRFamide (PEAK C) (CARDIOEXCITATORY NEUROPEPTIDE).
OS Macrocallista nimbosa (Sun-ray clam), Nereis virens (Sandworm),
OS Hirudo medicinalis (Medicinal leech), and Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
OC Veneroidae; Veneridae; Macrocallista.
NCBI_TaxID=6594, 6353, 6421, 27815;
KW SEQUENCE. AND SYNTHESIS.
PP SPECIES-M. nimbosa; TISSUE-Cerebral pedal, and Visceral ganglion;
RC MEDLINE-77215956; PubMed-877582;
RA Price D.A., Greenberg M.T.;
RT "Structure of a molluscan cardioexcitatory neuropeptide.";
RL Science 197:670-671(1977).
RN [12]
PP SPECIES-M. nimbosa; TISSUE-Ganglion;
RC SPECIES-M. nimbosa; TISSUE-Ganglion;
RA MEDLINE-78012038; PubMed-909875;
RA Price D.A., Greenberg M.J.;
RT "Purification and characterization of a cardioexcitatory neuropeptide from the central ganglia of a bivalve mollusc.";
RL Pref. Biochem. 7:261-281(1977)
RN [13]
PP SPECIES-N. virens;
RC SPECIES-N. virens;
RA MEDLINE-90259856; PubMed-2342992;
RA Krahnak K.G., Price D.A.;
RT "Authentic FMRFamide is present in the polychaete Nereis virens.";
RL Peptides 11:75-77(1990).
RN [4]
KW SEQUENCE.
RC SPECIES-H. medicinalis;

```

RX MEDLINE-92195954; PubMed 1686933;  
 RA Evans B.D., Pohl J., Karisotis M.A., Calabrese R.L.;  
 RI "Identification of Human Neuropeptides in the medicinal leech."  
 RL Peptides 12:897-908(1991).  
 RN [5]  
 RP SEQUENCE.  
 RC SPECTRAL ANALYSIS, TISSUE KIDNEY,  
 RA MEDLINE-9426417; PubMed-7917128;  
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
 RI "Peptide-related peptides from the kidney of the snail, Helisoma  
 RI trivolvis."  
 RL Peptides 15:41-46(1994).  
 CC -1- FUNCTION: MONOACTIV. CARBOXYTERMINAL SUBSTANCE PHARMACOLOGICAL  
 CC ACTIVITIES IN TIME ADAPTATION, INDUCTION, AND PERMEABILIZATION OF  
 CC CARDIAC CONTRACTION.  
 CC -1- SIMILARITY: BELONGS TO THE FAPP (PMPERAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 DR PIR: A01426; ECKR.  
 DR PIR: A60418; A60418.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 4 4 AMIDATION.  
 SO SEQUENCE 4 AA: 600 MW: 694069940000000 GRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;  
 Best Local Similarity 0.0%; Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
 DB 1 F 1  
 RESULT 12  
 RM01\_YEAST  
 ID RM01\_YEAST STANDARD; PRT: 4 AA.  
 AC P36515;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L1 (YMC1) (FRAGMENT).  
 GN MRPL1.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 CX NCBI\_Taxid=4932;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE-91265156; PubMed 206272;  
 RA Graham L., Graack H.-R., Kraft V., Choi T., Goldschmidt-Peliss S.,  
 RA Kitakawa M.;  
 RI "Extended N-terminal sequencing of proteins of the large ribosomal  
 RI subunit from yeast mitochondria."  
 RL FEBS Lett. 284:51-56(1991).  
 DR PIR: S17255; S17255.  
 DR SGD: L0002641; MRPL1.  
 KW Ribosomal protein; Mitochondrion.  
 FT NON\_TER 4 4  
 SO SEQUENCE 4 AA: 402 MW: 777183503000000 GRC64.

Query Match 0.0%; Score 0; DB 1; Length 4;  
 Best Local Similarity 0.0%; Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 X 1  
 DB 1 S 1  
 RESULT 13  
 TUF1\_HUMAN  
 ID TUF1\_HUMAN STANDARD; PRT: 4 AA.

AC P01858;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 01-JUL-2000 (Rel. 40, Last annotation update)  
 DE PHAGOCYTOSIS-STIMULATING PEPTIDE (TUF1STIN).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Gnathostomata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=72187087; PubMed-4112769;  
 RA Nishikawa K., Constantopoulos A., Salch P.S., Najjar V.A.;  
 RI "The characteristics, isolation and synthesis of the phagocytosis  
 RI stimulating peptide tufstin."  
 RL Biochem. Biophys. Res. Commun. 47:172-179(1972).  
 RN [2]  
 RP IMMUNOGLOBULIN CLASS.  
 RA MEDLINE-68091045; PubMed-4169272;  
 RA Fialdo B.V., Najjar V.A.;  
 RI "The physiological role of the lymphoid system VI The stimulatory  
 RI effect of leucophilin gamma globulin (leucokinin) on the phagocytic  
 RI activity of human polymorphonuclear leucocyte."  
 RL Biochemistry 6:3386-3392(1967).  
 CC -1- MISCELLANEOUS: AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE  
 CC CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE  
 CC MEMBRANE RELEASES THE ACTIVE PEPTIDE TUF1STIN FROM THE GAMMA CHAIN.  
 CC TUF1STIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC  
 CC ACTIVITY OF NEUTROPHILS.  
 DR PIR: A02147; A02147.  
 DR MIM: 191150;  
 SO SEQUENCE 4 AA: 501 MW: 7417632100000000 GRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;  
 Best Local Similarity 0.0%; Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
 DB 1 T 1  
 RESULT 14  
 AL14\_CARMA  
 ID AL14\_CARMA STANDARD; PRT: 5 AA.  
 AC P81817;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE CARCINOSTATIN 14.  
 OS Carcinus maenas (Common shore crab) (Crustacea)  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubranchiura; Portunoidae; Portunidae; Carcinus.  
 CX NCBI\_Taxid=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion.  
 RA MEDLINE=98121193; PubMed-9461295;  
 RA Duye H., Johnson A.H., Maestro T.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RI "Isolation and identification of multiple neuropeptides of the  
 RI allatostatin superfamily in the shore crab Carcinus maenas."  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD\_RES 5 5 AMIDATION (POTENTIAL).  
 SO SEQUENCE 5 AA: 506 MW: 6126765600000000 GRC64;

Query Match 0.0%; Score 0; DB 1; Length 5;

Best Local Similarity 0.08; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1

DB 1 Y 1

RESULT 15

BIOA\_CITEP ID BIOA\_CITEP STANDARD PRT 5 AA.

AC P13071;

BT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

UF 01-OCT-2000 (Rel. 40, Last annotation update)

DE ADENOSYLMETHIONINE-8-AMINO-7-OXONANONATE AMINOTRANSFERASE

(EC 2.6.1.62) (7.8-DIAMINO-PICARONIC ACID AMINOTRANSFERASE) (DAPA

DE AMINOTRANSFERASE) (FRAGMENT).

GN BIOA.

OS Citrobacter freundii.

OC Bacteria; Proteobacteria; gamma subdivision, Enterobacteriaceae,

OT Citrobacter.

OX NCBI\_TaxID:546;

RN 111

RP SEQUENCE FROM N.A.

KX MEDLINE 89006280; PubMed-2971595;

KA Shlun D., Campbell A.;

KT "Transcriptional regulation and gene arrangement of Escherichia coli,

Citrobacter freundii and Salmonella typhimurium biotin operons.";

KL Gene 67:203-211(1988).

CC -|- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-

OXONANONATE = S-ADENOSYL-4-METHYLTHIO-2-OXOBUTANOATE +

7,8-DIAMINONANONATE.

CC -|- COFACTOR: PYRIDOXAL PHOSPHATE.

CC -|- PATHWAY: BIOTIN BIOSYNTHESIS.

CC -|- SUBUNIT: HOMODIMER.

CC -|- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT

AMINOTRANSFERASES.

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

EMBL: M21922; -; NOT\_ANNOTATED\_CDS.

DB INTERPRO: IPR000974; -;

DR PROSITE: PS00660; AA\_TRANSFPR\_CLASS\_3; PARTIAL.

KW Biot in biosynthesis; Transferase; Aminotransferase;

KM Pyridoxal phosphate.

FT NON\_TER 5

NO SOURCE 5 AA; 582 MW; 6AABAB1A6F00000 CRC64;

Query Match

Best Local Similarity 0.08; Score 0; DB 1; Length 5;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1

DB 1 M 1

Search completed: September 30, 2001, 10:29:16  
Job time: 26 sec



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US-07-791-2140-24
Sequence 24, Application US/077912130
Patent No. 5409495
GENERAL INFORMATION:
APPLICANT: MORISITA, Hiideaki
APPLICANT: KANAMORI, Toshiohri
TITLE OF INVENTION: POLYMERIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PROTECTING THE SAME, AND ENZYME
TITLE OF INVENTION: TRAITING USING THE SAME
TITLE OF INVENTION: TRAITING USING THE SAME
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESS: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07791, 2130
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 2-406745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meulin, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/AGENT NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-791-2140-24
Query Match 0.0% Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conserved: 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
DB 1 C 1

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STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07791, 2140
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meulin, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/AGENT NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-791-2140-40
Query Match 0.0% Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conserved: 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
DB 1 C 1

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1 TELEFAX:
2 TELEX:
3 INFORMATION FOR SEQ ID NO: 57:
4 SEQUENCE CHARACTERISTICS:
5 LENGTH: 1 amino acid
6 TYPE: amino acid
7 STRANDEDNESS: single
8 TOPOLOGY: linear
9 FEATURE:
10 NAME/KEY: modified site
11 LOCATION:
12 IDENTIFICATION METHOD:
13 OTHER INFORMATION: Note: "Xaa is modified amino acid as
14 OTHER INFORMATION: described in specification"
15 US-08-174-365A-97

Query Match          0.00; Score 0; DB 1; Length 1;
Best Local Similarity 100.00; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 X 1
DB 1 X 1

RESULT 5
US-07-789-913-23
1 Sequence 23, Application US/07789913
2 Patent No. 555095
3 GENERAL INFORMATION:
4 APPLICANT: Miljanich, George P.
5 APPLICANT: Homersox, Stephen S.
6 APPLICANT: Fox, James A.
7 APPLICANT: Valentino, Karen L.
8 APPLICANT: Bittner, Robert S.
9 APPLICANT: Yamashiro, Donald H.
10 TITLE OF INVENTION: Delayed Treatment Method of Reducing
11 TITLE OF INVENTION: Ischemia Related Neuronal Damage
12 NUMBER OF SEQUENCES: 28
13 CORRESPONDENCE ADDRESS:
14 ADDRESSEE: Law Offices of Peter DeHlincet
15 STREET: 450 Cambridge Avenue, Suite 300
16 CITY: Palo Alto
17 STATE: CA
18 COUNTRY: USA
19 ZIP: 94306
20 COMPUTER READABLE FORM:
21 MEDIUM TYPE: floppy disk
22 COMPUTER: IBM PC compatible
23 OPERATING SYSTEM: pc-tos/ms-dos
24 SOFTWARE: Patentia Release #1.0, Version #1.25
25 CURRENT APPLICATION DATA:
26 APPLICATION NUMBER: US/07789,913
27 FILING DATE: 19911112
28 CLASSIFICATION: 514
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: US/07789,913
31 FILING DATE: 02-AUG-1990
32 PRIOR APPLICATION DATA:
33 APPLICATION NUMBER: US/07789,913
34 FILING DATE: 22-NOV-1989
35 ATTORNEY/AGENT INFORMATION:
36 NAME: Stratford, Carol A.
37 REGISTRATION NUMBER: 34,444
38 REFERENCE/JACKET NUMBER: 5865-0005.30
39 TELECOMMUNICATION INFORMATION:
40 TELEPHONE: (415) 324-0860
41 TELEFAX: (415) 324-0960
42 INFORMATION FOR SEQ ID NO: 24:
43 SEQUENCE CHARACTERISTICS:
44 LENGTH: 1 amino acids
45 TYPE: AMINO ACID

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1 TOPOLOGY: both
2 MOLECULE TYPE: peptide
3 HYPOTHETICAL: NO
4 ANTI-SENSE: NO
5 ORIGINAL SOURCE:
6 INDIVIDUAL ISOLATE: peptide fragment used in the claims
7 US-07-789-913-24

Query Match          0.00; Score 0; DB 1; Length 1;
Best Local Similarity 100.00; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 C 1

RESULT 6
US-07-789-913-25
1 Sequence 25, Application US/07789913
2 Patent No. 555095
3 GENERAL INFORMATION:
4 APPLICANT: Miljanich, George P.
5 APPLICANT: Homersox, Stephen S.
6 APPLICANT: Fox, James A.
7 APPLICANT: Valentino, Karen L.
8 APPLICANT: Bittner, Robert S.
9 APPLICANT: Yamashiro, Donald H.
10 TITLE OF INVENTION: Delayed Treatment Method of Reducing
11 TITLE OF INVENTION: Ischemia Related Neuronal Damage
12 NUMBER OF SEQUENCES: 28
13 CORRESPONDENCE ADDRESS:
14 ADDRESSEE: Law Offices of Peter DeHlincet
15 STREET: 450 Cambridge Avenue, Suite 300
16 CITY: Palo Alto
17 STATE: CA
18 COUNTRY: USA
19 ZIP: 94306
20 COMPUTER READABLE FORM:
21 MEDIUM TYPE: floppy disk
22 COMPUTER: IBM PC compatible
23 OPERATING SYSTEM: pc-tos/ms-dos
24 SOFTWARE: Patentia Release #1.0, Version #1.25
25 CURRENT APPLICATION DATA:
26 APPLICATION NUMBER: US/07789,913
27 FILING DATE: 19911112
28 CLASSIFICATION: 514
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: US/07561,766
31 FILING DATE: 02-AUG-1990
32 PRIOR APPLICATION DATA:
33 APPLICATION NUMBER: US/07440,094
34 FILING DATE: 22-NOV-1989
35 ATTORNEY/AGENT INFORMATION:
36 NAME: Stratford, Carol A.
37 REGISTRATION NUMBER: 34,444
38 REFERENCE/JACKET NUMBER: 5865-0005.10
39 TELECOMMUNICATION INFORMATION:
40 TELEPHONE: (415) 324-0860
41 TELEFAX: (415) 324-0960
42 INFORMATION FOR SEQ ID NO: 25:
43 SEQUENCE CHARACTERISTICS:
44 LENGTH: 1 amino acids
45 TYPE: AMINO ACID
46 MOLECULE TYPE: both
47 HYPOTHETICAL: NO
48 ANTI-SENSE: NO
49 ORIGINAL SOURCE:
50 INDIVIDUAL ISOLATE: peptide fragment used in the claims
51 US-07-789-913-25

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Query Match          0.0% Score 0: DB 1: Length 1:
Best Local Similarity 0.0% Prod. No. 0:
Matches 0: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

QY 1 X 1
DB 1 R 1

RESULT 7
US-08-049-794-25
Sequence 25, Application US/08049794
Patent No. 5587454
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SMITH, KATHLEEN
APPLICANT: VALENTINO, KAREN L.
APPLICANT: MILLANICH, GEORGE P.
TITLE OF INVENTION: METHODS OF PREVENTING ANALGESIA AND
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Law Offices of Peter Dehlinger
STREET: 450 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
RECORD TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08049794
FILING DATE: 1998-04-15
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-Dec-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/ASSIGNMENT NUMBER: 5965-0093, 30
TELEPHONE: (415) 524-0880
TELEFAX: (415) 524-0960
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: AMINO ACID
MOLECULE TYPE: linear
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 32
US-08-049-794-25

```

```

Sequence 25, Application US/08049794
Patent No. 5587454
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SMITH, KATHLEEN
APPLICANT: VALENTINO, KAREN L.
APPLICANT: MILLANICH, GEORGE P.
TITLE OF INVENTION: METHODS OF PREVENTING ANALGESIA AND
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Law Offices of Peter Dehlinger
STREET: 450 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
RECORD TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08049794
FILING DATE: 1998-04-15
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-Dec-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/ASSIGNMENT NUMBER: 5965-0093, 30
TELEPHONE: (415) 524-0880
TELEFAX: (415) 524-0960
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: AMINO ACID
MOLECULE TYPE: linear
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 32
US-08-049-794-25

```

```

Query Match          0.0% Score 0: DB 1: Length 1:
Best Local Similarity 0.0% Prod. No. 0:
Matches 0: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

QY 1 X 1
DB 1 R 1

RESULT 9
US-08-433-037-12
Sequence 12, Application US/08433017
Patent No. 5707828
GENERAL INFORMATION:
APPLICANT: Steekristina, Kotikanyadan
APPLICANT: Bart, Kathryn A.
APPLICANT: Hirtley, Russell A.
APPLICANT: Smith, Gregory P.
APPLICANT: Ischopp, David E.
TITLE OF INVENTION: EXPRESSION OF HUMAN GROWTH ARRESTIN IN
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:

```

```

ADDRESS: Seilly, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11540-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/66/433,637
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DIGITAL, FRANK S.
REGISTRATION NUMBER: 31,346
REFERENCE/WORKET NUMBER: 9108Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-1725
TELEX: 249 961 SANS DR
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-433-037-12

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Query Match: 0.0%; Score 0; DB 1; Length 1;
Host Local Similarity: 0.0%; Pctd. NO. 0;
Matches: 0; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;

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QY 1 X 1
DB 1 1 1

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RESULT 10
US-08-448-606-4
Sequence 4, Application US/08448606
Patent No. 572114
GENERAL INFORMATION:
APPLICANT: Abrahams n, Lars
APPLICANT: Holmsten, Erik
APPLICANT: Kallner U, Christina
APPLICANT: Lake, Mats
APPLICANT: Mikaelsson, sa
APPLICANT: Seilly, forsten
TITLE OF INVENTION: Peptide s. system for Protein A
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESS: Polley & Lardner, Vande Sande & Priestly
STREET: 1800 M Street N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: U.S.
ZIP: 20046
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,606
FILING DATE: 25-AUG-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 071/979,701/061

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FILING DATE: 09-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9203753-0
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Amelick, Burton A.
REGISTRATION NUMBER: 24,852
REFERENCE/WORKET NUMBER: 0151/20121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)331-7111
TELEFAX: (202) 293-6259
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-448-606-4

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Query Match: 0.0%; Score 0; DB 1; Length 1;
Host Local Similarity: 0.0%; Pctd. NO. 0;
Matches: 0; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;
QY 1 X 1
DB 1 0 1

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RESULT 11
US-07-869-933-16
Sequence 16, Application US/07869933
Patent No. 5770396
GENERAL INFORMATION:
APPLICANT: Kinet, Jean-pierre
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
TITLE OF INVENTION: IMMUNOGLOBULIN
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESS: Polley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BERT, Stephen A.
REGISTRATION NUMBER: 29,768
TELEPHONE: (703)836-9400
TELEFAX: (703)833-4109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)331-7111
TELEFAX: (202) 293-6259
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-869-933-16

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Query Match: 0.0%; Score 0; DB 1; Length 1;

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Best Local Similarity: 0.0%; Pred. No. 0;  
Matches: 0; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;

QY 1 X 1

Db 1 c 1

US-08-294-150A-24

Sequence 23, Application US/08294150A

Patent No. 5792629

GENERAL INFORMATION:

APPLICANT: MORISHITA, HIROAKI

APPLICANT: KAWABETA, Yoshitaka

APPLICANT: NISHIMURA, Masahiro

TITLE OF INVENTION: PEPTIDES, DNA FRAGMENT ENCODING THE SAME, AND ENZYME

TITLE OF INVENTION: SAME AND PROCESS FOR IMPROVING THE SAME, AND ENZYME

TITLE OF INVENTION: IDENTIFICATION PROCESS, TEST COMPOSITION AND METHODS OF

NUMBER OF SEQUENCE: 110

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DWANE, SWICKER & MATHIS

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22304-1404

COMPIER READABLE FORM:

MODERN TYPE: floppy disk

MODIFIER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 03/79791, 213

FILING DATE: 19-AUG-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 02/67791, 213

FILING DATE: 14-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 2-096745

FILING DATE: 14-NOV-1990

ATTORNEY/AGENT INFORMATION:

NAME: Morith, Hiroaki M.

REGISTRATION NUMBER: 46,607

REFERENCE/AGENT NUMBER: 020650 949

TELEPHONE: (703) 846 6620

TELEFAX: (703) 846-2021

INVENTION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 1 amino acids

TYPE: amino acid

Topology: linear

MOLECULE TYPE: peptide

US-08-294-150A-24

APPLICANT: MORISHITA, HIROAKI

APPLICANT: KAWABETA, Yoshitaka

APPLICANT: NISHIMURA, Masahiro

TITLE OF INVENTION: PEPTIDES, DNA FRAGMENT ENCODING THE

TITLE OF INVENTION: SAME AND PROCESS FOR IMPROVING THE SAME, AND ENZYME

TITLE OF INVENTION: IDENTIFICATION PROCESS, TEST COMPOSITION AND METHODS OF

NUMBER OF SEQUENCE: 110

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DWANE, SWICKER & MATHIS

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22304-1404

COMPIER READABLE FORM:

MODERN TYPE: floppy disk

MODIFIER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 03/79791, 213

FILING DATE: 19-AUG-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 02/67791, 213

FILING DATE: 14-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 2-096745

FILING DATE: 14-NOV-1990

ATTORNEY/AGENT INFORMATION:

NAME: Morith, Hiroaki M.

REGISTRATION NUMBER: 46,607

REFERENCE/AGENT NUMBER: 020650-049

TELEPHONE: (703) 846 6620

TELEFAX: (703) 846 2021

INVENTION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 1 amino acids

TYPE: amino acid

Topology: linear

MOLECULE TYPE: peptide

US-08-294-150A-40

QY 1 X 1

Db 1 c 1

US-08-496-847-23

Sequence 23, Application US/08496847

Patent No. 5795864

GENERAL INFORMATION:

APPLICANT: AMSTUTZ, Gary A.

APPLICANT: BOWSTON, Stephen S.

APPLICANT: SCHILL, Kishorchandra

APPLICANT: Adilansous, Peter L.

APPLICANT: Kristipati, Ramasharma

TITLE OF INVENTION: METHODS AND

TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROLIFERATION OF BRUSSELLA PAIN

NUMBER OF SEQUENCE: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: 350 Cambridge Avenue, Suite 250

CITY: Palo Alto

STATE: CA

COUNTRY: US  
 ZIP: 94306-1546  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION NUMBER: 95032496,847  
 FILING DATE: 27-JUN-1995  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Stratford, Carol A  
 REGISTRATION NUMBER: 34,444  
 RETIREMENT/STATUS NUMBER: 0905, 0009, 31  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-324-0880  
 TELEFAX: 650-324-0960  
 INFORMATION FOR SEQ ID NO: 21:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ORIGINAL SOURCE:  
 INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT  
 US-09-498-847-24

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 Host Local Similarity 0.0% Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
 DB 1 C 1

Result 15  
 US-09-498-847-25  
 Sequence 25, Application US/09498847  
 Patient No. 5795864  
 GENERAL INFORMATION:  
 APPLICANT: Amstutz, Gary A.  
 APPLICANT: Bokorsov, Stephen S.  
 APPLICANT: Gohil, Kishorshandra  
 APPLICANT: Ahlhaussens, Peter I.  
 APPLICANT: Kristipati, Ramasharma  
 TITLE OF INVENTION: MITH-OS AND  
 NUMBER OF SEQUENCES: 46  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Daulton & Associates  
 STREET: 450 Cambridge Avenue, Suite 250  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: US  
 ZIP: 94306-1546  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 95032496,847  
 FILING DATE: 27-JUN-1995  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Stratford, Carol A  
 REGISTRATION NUMBER: 34,444  
 REFERENCE/SEQID NUMBER: 5845-0009, 41  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-324-0880  
 TELEFAX: 650-324-0960  
 INFORMATION FOR SEQ ID NO: 25:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ORIGINAL SOURCE:  
 INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT  
 US-09-498-847-25

Query Match 0.0% Score 0; DB 1; Length 1;  
 Host Local Similarity 0.0% Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 X 1  
 DB 1 R 1

Search completed: September 30, 2001, 10:29:48  
 Job Time: 48 sec

Sun Sep 30 10:33:18 2001

us-09-498-556-85.rai

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Page 8

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

• protein - protein search, using sw model

Septemher 40, 2001, 10:40:46 ; Search time 2.59 seconds

(MILITARY) 16-20 MILITARY

US-44-4148 556-889

**Schäffer, J. C.** 1987. **Xxxxxx**

Scoring table: **BLISSIM62**

Submitted: 425024 0011, 127295027 received

total number of hits satisfying chosen parameters: 425026

Maximum job seq length: 20000000000

Post-processing: Minimum March 08

List of Lists 45

[illegible]

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2: SP_Asteraceae: *
3: SP_Boraginaceae: *
4: SP_Polemoniaceae: *
5: SP_Berberidaceae: *
6: SP_Menyanthes: *
7: SP_Umbelliferae: *
8: SP_Corvaceae: *
9: SP_Phagelium: *
10: SP_Pulsatilla: *
11: SP_Polemonium: *
12: SP_Menyanthes: *
13: SP_Asteraceae: *
14: SP_Polemoniaceae: *

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARY

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2	0	0.6	5	10	0.9407	0.9497	hordum contig
4	0	0.0	5	13	0.83070	0.84070	ilicoria root
4	0	0.0	5	13	0.83871	0.84871	ilicoria root
5	0	0.0	5	13	0.84072	0.85072	ilicoria root
6	0	0.0	5	13	0.85073	0.86073	ilicoria root
7	0	0.0	5	13	0.82099	0.83099	ilicoria root
8	0	0.0	5	13	0.82100	0.83100	ilicoria root
9	0	0.6	6	4	0.82655	0.83655	ilicoria root
10	0	0.6	6	4	0.08720	0.08720	homo sapiens
11	0	0.0	6	10	0.82181	0.83181	ilicoria root
12	0	0.0	6	10	0.82182	0.83182	ilicoria root
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14	0	0.6	6	13	0.82066	0.83066	ilicoria root
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16	0	0.0	7	2	0.07451	0.07451	synecchococcus
17	0	0.0	7	2	0.84028	0.84028	pseudomonas
18	0	0.0	7	2	0.47029	0.47029	eretrobacter
19	0	0.0	7	2	0.78004	0.78004	eretrobacter

## ALIGNMENT

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21	0	0.0	7	2	O50556	ostriobacill
22	0	0.0	7	2	Q47505	eschschia
23	0	0.0	7	2	Q47477	eschschia
24	0	0.0	7	4	Q15897	homo sapien
25	0	0.0	7	4	Q15903	homo sapien
26	0	0.0	7	6	Q28742	cytolasus
27	0	0.0	7	8	P92421	psaliyrosta
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29	0	0.0	7	8	P92210	artofrod c
30	0	0.0	7	8	P92214	amblyoprym
31	0	0.0	7	8	P92218	amblyoprym
32	0	0.0	7	8	P92221	amblyoprym
33	0	0.0	7	8	P92226	homo ther
34	0	0.0	7	8	P92372	heymadla v
35	0	0.0	7	8	P92381	hordum bra
36	0	0.0	7	8	P92387	hordum bra
37	0	0.0	7	8	P92390	nercardia l
38	0	0.0	7	8	P92392	hordum v.11
39	0	0.0	7	8	P92425	hordum v.11
40	0	0.0	7	8	P92427	isodurecyon
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42	0	0.0	7	8	P92442	isodurecyon
43	0	0.0	7	8	P92440	isodurecyon
44	0	0.0	7	8	P92445	isodurecyon
45	0	0.0	7	10	P93233	lyopetsicoc

RESULT	1
Q68433	
AP	UP04333
AC	UP04333
DT	01-NOV-1996 (TREMBL) , 01, Created)
DE	01-NOV-1996 (TREMBL) , 01, Last sequence update)
DI	01-JAN-1999 (TREMBL) , 09, Last annotation update)
DEF	GMP-GLYCINE N-SYTLTRANSFERASE, MICROBIAL; [EC 2.4.1.17] (MGG1)
ID	[FRAGMENT].
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OF	Mammalia; Eutheria; Rodentia; Sittimorphii; Muridae; Murinae; Ratto-
OX	Nobis_Loxip:10116;
XN	[1]
FE	SEQUENCE FROM N.A.
RE	STRAIN-GINS:
EX	M3A-HU-91282758; PubMed 1840486;
KA	Sato H., Aono S., Kashimatsu S., Koike O.;
RI	"Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RL	hypochlorhydric Gunn rat";
RT	Biochem Biophys Res Commun. 177(116):1144(1991).
CC	-1- PURIFIER: OBJECT IS OF MAJOR IMPORTANCE IN THE CO-REGULATED AND
CZ	SUBSTRATE IN REGULATION OF ENZYMICITY AND KINETICS FOR AND
CV	ENZYME(S) IN GINS.
CS	-1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC	HEXA-D-GLUCONOSIDE.
CC	-1- SPECIFIC LIGATION: MICROSCOPIC.
FB	EBHL 68626; AA019259,1 - "
FZ	Transferrase, glycosyltransferase; Microsome; Multigene family.
FI	NON_ITER 1 4
FI	NON_ITER 4 4
NC	SEQUENCE 4 AA, 473 MW, 633792.420000000 MOGS;

Query Match: 0.00; Score 0; DB 11; Length 4;  
 Best Local Similarity: 0.00; Pred. No. 0;  
 Matches: 0; Conservative: 0; Mismatches: 1; Indels: 0;  
 Gaps: 0

121

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Query Match          0.08; Score 0; Hit 13; Length 5;
Host Local Similarity 0.08; Prod. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY      1 X 1
DB      1 V 1

RESULT 4
PR2071
PR2071      PRELIMINARY; FRT; 5 AA.
01-MAY-2000 (ITERM001, 13, Created)
01-MAY-2000 (ITERM001, 13, Last sequence update)
01-MAY-2000 (ITERM001, 13, Last annotation update)
RUBELIDIN 2.1.
Litoria rubella (Desert Tree Frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Buianoidae; Hyliidae;
Litoria.
NCBI_TaxID:104895;
RN      111
SEQUENCE AND MASS SPECTROMETRY.
RT      TISSUE=SKIN SECTION.
RA      Steinbocker S.L., Watson P.A., Wauth R.J., Howie J.H., Guo Q.,
RA      Taylor M.J., Wallace J.C.;
RT      "The structure of new peptides from the Australian red tree frog
RT      Litoria rubella: the skin peptide profile as a probe for the study
RT      of evolutionary trends of amphibians."
RL      Aust. J. Zool., 49:955-963(1999).
RN      1
FUNCTION: CHARACTERISES NEW PEPTIDE ACTIVITY FOR
CY      -1- ANTIBIOTIC ACTIVITY.
CY      -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN LOUSAL GLANDS.
CY      -1- MASS SPECTROMETRY: MW=626; METHOD FAB.
KW      Amphibian skin.
SD      SEQUENCE: 5 AA: 626 MW: 94809.96 POSITIVELY CHARGED;

Query Match          0.08; Score 0; Hit 13; Length 5;
Host Local Similarity 0.08; Prod. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY      1 X 1
DB      1 V 1

RESULT 5
PR2072
PR2072      PRELIMINARY; FRT; 5 AA.
01-MAY-2000 (ITERM001, 13, Created)
01-MAY-2000 (ITERM001, 13, Last sequence update)
01-MAY-2000 (ITERM001, 13, Last annotation update)
RUBELIDIN 4.1.
Litoria rubella (Desert Tree Frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Buianoidae; Hyliidae;
Litoria.
NCBI_TaxID:104895;
RN      111
SEQUENCE AND MASS SPECTROMETRY.
RT      TISSUE=SKIN SECTION.
RA      Steinbocker S.L., Watson P.A., Wauth R.J., Howie J.H., Guo Q.,
RA      Taylor M.J., Wallace J.C.;
RT      "The structure of new peptides from the Australian red tree frog
RT      Litoria rubella: the skin peptide profile as a probe for the study
RT      of evolutionary trends of amphibians."
RL      Aust. J. Zool., 49:955-963(1999).
RN      1
FUNCTION: CHARACTERISES NEW PEPTIDE ACTIVITY FOR
CY      -1- ANTIBIOTIC ACTIVITY.
CY      -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN LOUSAL GLANDS.
CY      -1- MASS SPECTROMETRY: MW=626; METHOD FAB.
KW      Amphibian skin.
SD      SEQUENCE: 5 AA: 626 MW: 94809.96 POSITIVELY CHARGED;

```



## ANTIBIOTIC ACTIVITY

CV -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN GLANDS. CLANES.  
 KW -1- MASS SPECITOMETRIC: MW 655; MELTD 148.  
 FT Amphibian skin; Amidatide.  
 ST MOD RES 5 AA: 556 MW: 71A9C9CB10340000 CRO64;  
 SQ SEQUENCE 5 AA: 556 MW: 71A9C9CB10340000 CRO64;

Query Match 0.08; Score 0; DB 13; Length 5;  
 Best Local Similarity 0.08; Pred. No. 0;  
 Matches 0; Conservation 0; Mismatches 1; Indels 0; Gaps 0;

UY 1 X 1  
 DB 1 F 1

## RESULT 6

PR2073 PRELIMINARY: PRT: 5 AA.

DI 01-MAY-2000 (TREMUR: 13, Created)  
 DT 01-MAY-2000 (TREMUR: 13, last sequence update)  
 DE 01-MAY-2000 (TREMUR: 13, last annotation update)  
 DE RUBELLIN 4.2.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;  
 OC Litoria.  
 OX Nhl\_TaxID:16495;  
 RN 11  
 RP SEQUENCE.  
 RC TISSUE SKIN SECRETION.  
 KA Madrilis P.A., Bowle J.H., Tyler M.J., Wallace J.C.,  
 FT "Peptides from the skin glands of the Australian Popping tree frog  
 RT Litoria rubella." Comparison with the skin peptides from Litoria  
 rubella."  
 RL Aust. J. Chem. 52:0-0(1999).  
 CC -1- FUNCTION: CAPRINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
 CC ANTIBIOTIC ACTIVITY.  
 CV -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
 KW Amphibian skin.  
 ST MOD RES 5 AA: 570 MW: 71A9C9CB2A0000 CRO64;  
 SQ SEQUENCE 5 AA: 570 MW: 71A9C9CB2A0000 CRO64;

Query Match 0.08; Score 0; DB 13; Length 5;  
 Best Local Similarity 0.08; Pred. No. 0;  
 Matches 0; Conservation 0; Mismatches 1; Indels 0; Gaps 0;

UY 1 X 1  
 DB 1 V 1

## RESULT 7

PR2099 PRELIMINARY: PRT: 5 AA.

DI 01-MAY-2000 (TREMUR: 13, Created)  
 DT 01-MAY-2000 (TREMUR: 13, last sequence update)  
 DE 01-MAY-2000 (TREMUR: 13, last annotation update)  
 DE ELECTRIN 4.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;  
 OC Litoria.  
 OX Nhl\_TaxID:16495;  
 RN 11  
 RP SEQUENCE.  
 RC TISSUE SKIN SECRETION.  
 KA Madrilis P.A., Bowle J.H., Tyler M.J., Wallace J.C.,  
 FT "Peptides from the skin glands of the Australian Popping tree frog  
 RT Litoria rubella." Comparison with the skin peptides from Litoria

RT rubella."  
 RL Aust. J. Chem. 52:0-0(1999).  
 KW Amphibian skin; Amidatide.  
 FT MOD RES 5 AA: 556 MW: 66A761F2C9A00000 CRO64;  
 SQ SEQUENCE 5 AA: 556 MW: 66A761F2C9A00000 CRO64;

Query Match 0.08; Score 0; DB 13; Length 5;  
 Best Local Similarity 0.08; Pred. No. 0;  
 Matches 0; Conservation 0; Mismatches 1; Indels 0; Gaps 0;

UY 1 X 1  
 DB 1 F 1

## RESULT 8

PR2100 PRELIMINARY: PRT: 5 AA.

DI 01-MAY-2000 (TREMUR: 13, Created)  
 DT 01-MAY-2000 (TREMUR: 13, last sequence update)  
 DE 01-MAY-2000 (TREMUR: 13, last annotation update)  
 DE ELECTRIN 4.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;  
 OC Litoria.  
 OX Nhl\_TaxID:16495;  
 RN 11  
 RP SEQUENCE.  
 RC TISSUE SKIN SECRETION.  
 KA Madrilis P.A., Bowle J.H., Tyler M.J., Wallace J.C.,  
 FT "Peptides from the skin glands of the Australian Popping tree frog  
 RT Litoria rubella." Comparison with the skin peptides from Litoria  
 rubella."  
 RL Aust. J. Chem. 52:0-0(1999).  
 CC -1- FUNCTION: CAPRINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
 CC ANTIBIOTIC ACTIVITY.  
 CV -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
 KW Amphibian skin.  
 ST MOD RES 5 AA: 616 MW: 61F2D1A05A0000 CRO64;  
 SQ SEQUENCE 5 AA: 616 MW: 61F2D1A05A0000 CRO64;

Query Match 0.08; Score 0; DB 13; Length 5;  
 Best Local Similarity 0.08; Pred. No. 0;  
 Matches 0; Conservation 0; Mismatches 1; Indels 0; Gaps 0;

UY 1 X 1  
 DB 1 F 1

## RESULT 9

PR2655 PRELIMINARY: PRT: 6 AA.

DI 01-MAR-2001 (TREMUR: 16, Created)  
 DT 01-MAR-2001 (TREMUR: 16, last sequence update)  
 DE 01-MAR-2001 (TREMUR: 16, last annotation update)  
 DE ACID SHOCK PROTEIN (PASCENT)  
 OS Lactobacillus sanfranciscensis (Lactobacillus sanfranciscensis).  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;  
 OC Lactobacillus.  
 OX Nhl\_TaxID:1625;  
 RN 11  
 RP SEQUENCE.  
 RC STRAIN CBI.  
 KA De Angelis M., Rini L., Pallini V., Gobbelli M.,  
 FT "The acid stress response in Lactobacillus sanfranciscensis."  
 CC 1 INDUCTION, OVEREXPRESSED IN ACID ENVIRONMENTS.  
 FT MOD RES 6 AA: 778 MW: 6A4F56B72A5200 T-94;  
 SQ SEQUENCE 6 AA: 778 MW: 6A4F56B72A5200 T-94;

Query Match: 0.0%; Score 0; DB 2; Length 6;  
 Best Local Similarity: 100.0%; Ident. No. 0;  
 Matches: 1; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0;

UY 1 X 1  
 DB 1 X 1

RESULT 10  
 GDB#20  
 ID: 008720 PRELIMINARY: PRT: 6 AA.  
 AC: 008720:  
 DT: 01-NOV-1996 (TREMBOLO: 01, created)  
 DI: 01-NOV-1996 (TREMBOLO: 01, last sequence update)  
 DE: 01-NOV-1998 (TREMBOLO: 05, last annotation update)  
 DE: Y PROTEIN (TKAMENI).  
 GN: CREB.  
 OS: Homo sapiens (human).  
 OC: Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC: Mammalia; Eutheria; Primates; Catartida; Homalidae; Homo;  
 NC: NTL:taxid:9606.  
 LN: 11  
 KF: SEQUENCE FROM N.A.  
 RX: MEDLINE 0010601; PubMed 136444;  
 RA: Wootton G., Edmonson J.E.;  
 RT: "Novel testis germ cell-specific transcript of the *Creb* gene encodes an alternatively spliced exon with multiple in-frame stop codons.";  
 RI: Endocrinology 141:2010-2015(1992).  
 DI: PMID: 869994; CAA8780.1; .  
 DE: N-TER 1  
 FT: N-TER 6  
 ST: SEQUENCE 6 AA: 675 MW: 67228.627 kDa; T654.

Query Match: 0.0%; Score 0; DB 4; Length 6;  
 Best Local Similarity: 0.0%; Ident. No. 0;  
 Matches: 0; Conserved: 0; Mismatches: 1; Indels: 0; Gaps: 0;

UY 1 X 1  
 DB 1 S 1

RESULT 11  
 GDB#1  
 ID: P82181 PRELIMINARY: PRT: 6 AA.  
 AC: P82181:  
 DT: 01-JUN-2000 (TREMBOLO: 14, created)  
 DI: 01-JUN-2000 (TREMBOLO: 14, last sequence update)  
 DE: 01-MAR-2001 (TREMBOLO: 16, last annotation update)  
 DE: CHLOROPLAST 50S RIBOSOMAL PROTEIN L10 BETA (FRAGMENT).  
 OS: Spirochaetaceae (Spirocha).  
 OC: Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC: Magnoliophyta; Eudicotyledons; Core eudicot; Caryophyllales;  
 OC: Caryophyllales; Chelodactylaceae; Spirocha.  
 NC: NTL:taxid:5662.  
 LN: 11  
 KF: SEQUENCE.  
 RX: STRAIN CV. ALMAHO; TISSUE LEAF;  
 RA: YAMAMOTO K., SUZUKAWA A.R.;  
 RT: "The plastid ribosomal proteins: identification of all the proteins in the 50S subunit of an ornamental ribosome (chloroplast).";  
 RI: J. Biol. Chem. 275:28466-28482(2000).  
 DE: 01-MAR-2001 (TREMBOLO: 16, last annotation update)  
 DE: CHLOROPLAST 50S RIBOSOMAL PROTEIN L10 BETA (TKAMENI).  
 GN: Spirochaetaceae (Spirocha).  
 OS: Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC: Magnoliophyta; Eudicotyledons; Core eudicot; Caryophyllales;  
 OC: Caryophyllales; Chelodactylaceae; Spirocha.  
 NC: NTL:taxid:5662.  
 LN: 11  
 KF: SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RX: STRAIN CV. ALMAHO; TISSUE LEAF;

KW Ribosomal protein: chloroplast; rRNA-binding.  
 FT N-TER 6  
 ST SEQUENCE 6 AA: 675 MW: 64218.415 kDa; T6544.

Query Match: 0.0%; Score 0; DB 10; Length 6;  
 Best Local Similarity: 0.0%; Ident. No. 0;  
 Matches: 0; Conserved: 0; Mismatches: 1; Indels: 0; Gaps: 0;

UY 1 X 1  
 DB 1 A 1

RESULT 12  
 GDB#182  
 ID: P82182 PRELIMINARY: PRT: 6 AA.  
 AC: P82182:  
 DT: 01-JUN-2000 (TREMBOLO: 14, created)  
 DI: 01-JUN-2000 (TREMBOLO: 14, last sequence update)  
 DE: 01-MAR-2001 (TREMBOLO: 16, last annotation update)  
 DE: CHLOROPLAST 50S RIBOSOMAL PROTEIN L10 GAMMA (TKAMENI).  
 OS: Spirochaetaceae (Spirocha).  
 OC: Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC: Magnoliophyta; Eudicotyledons; Core eudicot; Caryophyllales;  
 OC: Caryophyllales; Chelodactylaceae; Spirocha.  
 NC: NTL:taxid:5662.  
 LN: 11  
 KF: SEQUENCE.  
 RX: STRAIN CV. ALMAHO; TISSUE LEAF;  
 RA: MEDLINE 20435798; PubMed 1087046;  
 RA: YAMAMOTO K., SUZUKAWA A.R.;  
 RT: "The plastid ribosomal proteins: identification of all the proteins in the 50S subunit of an ornamental ribosome (chloroplast).";  
 RI: J. Biol. Chem. 275:28466-28482(2000).  
 DE: 01-MAR-2001 (TREMBOLO: 16, last annotation update)  
 DE: CHLOROPLAST 50S RIBOSOMAL PROTEIN L10 GAMMA (TKAMENI).  
 GN: Spirochaetaceae (Spirocha).  
 OS: Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC: Magnoliophyta; Eudicotyledons; Core eudicot; Caryophyllales;  
 OC: Caryophyllales; Chelodactylaceae; Spirocha.  
 NC: NTL:taxid:5662.  
 LN: 11  
 KF: SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RX: STRAIN CV. ALMAHO; TISSUE LEAF;

Query Match: 0.0%; Score 0; DB 10; Length 6;  
 Best Local Similarity: 0.0%; Ident. No. 0;  
 Matches: 0; Conserved: 0; Mismatches: 1; Indels: 0; Gaps: 0;

UY 1 X 1  
 DB 1 A 1

RESULT 13  
 GDB#41  
 ID: P82541 PRELIMINARY: PRT: 6 AA.  
 AC: P82541:  
 DT: 01-OCT-2000 (TREMBOLO: 15, created)  
 DI: 01-OCT-2000 (TREMBOLO: 15, last sequence update)  
 DE: 01-MAR-2001 (TREMBOLO: 16, last annotation update)  
 DE: CHLOROPLAST 50S RIBOSOMAL PROTEIN L10 BETA (TKAMENI).  
 OS: Spirochaetaceae (Spirocha).  
 OC: Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC: Magnoliophyta; Eudicotyledons; Core eudicot; Caryophyllales;  
 OC: Caryophyllales; Chelodactylaceae; Spirocha.  
 NC: NTL:taxid:5662.  
 LN: 11  
 KF: SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RX: STRAIN CV. ALMAHO; TISSUE LEAF;

KX MEDLINE:20435707; PubMed:10874039;  
 KA Yamamoto K., von Knochlauch K., Supramanian A.R.;  
 KI "The plastid ribosomal proteins: Identification of all the proteins in  
 K1 the small subunit of an organelle ribosome (chloroplast)";  
 KJ J. Biol. Chem. 273:28455-28465(2000).  
 KL -1 FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.  
 KM -1 SUBCELLULAR LOCATION: CHLOROPLAST.  
 KN -1 CDSER SEQUENCE: EXPRESSED IN ALL PLANT TISSUES.  
 KO MASS SPECTROMETRY: MW:10477.0; METHOD ELECTROSPRAY.  
 KP MASS SPECTROMETRY: MW:10475.0; METHOD ELECTROSPRAY.  
 KQ MISCELLANEOUS: SIX ALPHA AND BETA FORMS DIFFER IN THE SIX BETA  
 KR FORM IS THE MINOR BASIC FORM.  
 KS -1 MISCELLANEOUS: ON THE 2D-GEL, THE MW IS: 12 KDA.  
 KT -1 SIMILARITY: HOMONS TO THE S19 FAMILY OF RIBOSOMAL PROTEINS.  
 KU InterPro: IPR002222;  
 KV PROSITE: PS00127; RIBOSOMAL\_S19; PARTIAL  
 KW Ribosomal protein: chloroplast; RNA-binding.  
 KX N\_NTER 6  
 KY SEQUENCE 6 AA: 792 MW: 6333376A4110006 CRC64;  
 SZ

Query Match 0.08; Score 0; DB 10; Length 6;  
 Best local Similarity 0.08; Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
 DB 1 T 1

RESULT 14  
 PRT 06  
 TL 192096 PRELIMINARY: PRT: 6 AA.  
 AT 192096;  
 DI 01-MAY-2000 (TEMPREL: 13, Created)  
 DI 01-MAY-2000 (TEMPREL: 13, Last sequence update)  
 DI 01-MAY-2000 (TEMPREL: 13, Last annotation update)  
 DE ELECTRIN 1.  
 OS Litoria rubella (Poison free frog).  
 KS Eukaryota; Metazoa; Chordata; Creatura; Vertebrata; Entelostomi;  
 KU Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 KW Litoria;  
 KX NTER:1axfu:104895;  
 KY N 1;  
 RP SEQUENCE:  
 RP TISSUE:SKIN SECRETION;  
 KA Wainitz E.A., Howie J.H., Tyler M.J., Wallace J.C.;  
 KI "Proteins from the skin glands of the Australian buzzy tree frog  
 K1 Litoria electrica: Comparison with the skin peptides from Litoria  
 K1 rubella";  
 KL Aust. J. Chem. 52:9-10(1999).  
 KW Amphibian skin; Amidation.  
 KT M\_TER 6  
 KY SEQUENCE 6 AA: 792 MW: 658376477239A000 CRC64;  
 SZ

Query Match 0.08; Score 0; DB 13; Length 6;  
 Best local Similarity 0.08; Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
 DB 1 F 1

RESULT 15  
 TL 254248 PRELIMINARY: PRT: 7 AA.  
 AT 254248;  
 DI 01-NOV-1996 (TEMPREL: 01, Created)  
 DI 01-NOV-1996 (TEMPREL: 01, Last sequence update)  
 DI 01-NOV-1996 (TEMPREL: 01, Last annotation update)  
 DE SPOY & ADK GINES (FRAGMENT).

GN RELI.  
 OS Streptomyces griseus.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomyces; Streptomyces; Streptomyces;  
 OX NCBI:taxid:1911;  
 RN 11;  
 RP SEQUENCE FROM N.A.  
 KC STRAIN: N2-3-11;  
 KA Pochlitz S., Piepersberg W., Wehner U.P.;  
 KI Subtilisin (Fes 1946) from the SWF55-05b and J100J databases.  
 KR EMBL: X95915; CAA65160.1;  
 KT N\_NTER 1  
 KY SEQUENCE 7 AA: 760 MW: 72672601B01B2A0 CRC64;  
 SZ

Query Match 0.08; Score 0; DB 2; Length 7;  
 Best local Similarity 0.08; Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
 DB 1 V 1

Search completed: September 30, 2001, 10:30:47  
 Job time: 117 sec







P1 Bertram PM, Gansseman YOL, Jespers LS, Laroche YR,  
 P1 Lauwereys MJ, Messens JHL, Moyle M, Stanssens PH;  
 P1 Vlasuk GP;  
 XX  
 DR WP1: 1996-22007/22;  
 DR N-PSDB; AAT12947;  
 XX  
 P1 Proteolysis with anticomplement and/or serine protease inhibitory  
 P1 activity - isolated from nematodes and useful to inhibit blood  
 P1 coagulation  
 PS  
 PS Claim 89 + 96, Fig 9, 24pp, English.  
 CC  
 CC Proteins with anticoagulant and/or serine protease inhibitory  
 CC activity, isolated from nematodes, are useful to inhibit blood  
 CC coagulation. The proteins can be added to blood collection tubes  
 CC defining the collection of mammalian plasma. They are also useful  
 CC to prevent or inhibit thrombosis, and may be given alone or in  
 CC combination with other therapeutic or in vivo diagnostic agents.  
 CC The proteins can serve as immunogens to raise antibodies for use in  
 CC the diagnosis and identification of NAP concn. levels in biological  
 CC fluids, e.g. to detect mammalian infection with a parasitic worm.  
 CC They can also be used as immunogens in prophylactic and therapeutic  
 CC vaccines against parasitic worm infection. The proteins may  
 CC deactivate the clotting time of human plasma in prothrombin time assays  
 CC when present at 10-50 nmol, and double the clotting time of human  
 CC plasma in activated partial thrombin time assays when present  
 CC at 10-100 nmol.  
 CC The anticoagulant proteins are pref. derived from  
 CC *Ancylostoma caninum*, *A. ceylanicum*, *A. dirdenale*, *Necator*  
 CC *americanus* or *Heligmosomoides polygyrus*.  
 CC The proteins first have 2 NAP domains and specifically inhibit  
 CC the catalytic activity of the factor VIIa/TF complex in the  
 CC presence of factor Xa or a catalytically inactive factor Xa deriv.,  
 CC do not specifically inhibit the activation of factor VIIa in the  
 CC absence of TF and do not specifically inhibit prothrombinase  
 XX  
 XX Sequence 91 AA.  
 S0  
 Query Match 100.0%; Score 486; DB 17; Length 91;  
 Host Local Similarity 100.0%; Pred. No. 66-39;  
 Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KATMGCGENFYVSTGSKETKTKKIVGVFFHFFHFNVPCTVWVHGVVPEGVFNK 50  
 Lp 8 KATMGCGENFYVSTGSKETKTKKIVGVFFHFFHFNVPCTVWVHGVVPEGVFNK 67  
 QY 61 DDKCVSAEDCELDMDPIYPTNRN 84  
 DB 68 ddkcvsaedcelmdmdfipyptnrn 91  
 RESULT 4  
 AAY30393  
 ID AAY30393 standard; Protein; 91 AA.  
 AC AAY30393;  
 XX  
 XX 15-NOV-1999 (first entry)  
 DE Nematode extracted anticoagulant protein *AcanNAPc2*.  
 XX  
 XX Nematode extracted anticoagulant protein; NAP; anticoagulant;  
 KW serine protease inhibitor; NAP domain; factor VIIa/TF.  
 XX  
 XX *Ancylostoma caninum*.  
 OS  
 XX US9595294-A  
 FN  
 XX 21-SEP-1999.  
 PD  
 XX 19-APR-1996; 96US-0634041.  
 PF

XX  
 PR 19-APR-1996; 96US-0634041.  
 PR 18-OCT-1994; 94US-0326110.  
 PR 05-JUN-1995; 95US-0461965.  
 PR 05-JUN-1995; 95US-0465980.  
 PR 05-JUN-1995; 95US-0486397.  
 PR 05-JUN-1995; 95US-0486399.  
 PR 17-OCT-1995; 95US-0486399.  
 XX  
 XX (CORV-) CORVAS INT INC.  
 XX  
 P1 Bertram PM, Gansseman YOL, Jespers LS, Laroche YR,  
 P1 Lauwereys MJ, Messens JHL, Moyle M, Stanssens PH;  
 P1 Vlasuk GP;  
 XX  
 DR WP1: 1996-22007/22;  
 DR N-PSDB; AAZ99999.  
 XX  
 XX Screening an isolated protein for Nematode extracted Anticoagulant  
 XX protein domains  
 XX  
 XX Example 13; Fig 9; 197pp; English.  
 CC The present sequence represents a nematode extracted anticoagulant  
 CC protein (NAP). The protein has activity as an anticoagulant and/or serine  
 CC protease inhibitor. The protein contains at least one NAP domain which  
 CC has selective inhibitory activity for factor VIIa/TF. The specification  
 CC describes a method for screening an isolated protein at least one domain  
 CC for factor VIIa/TF selective inhibitory activity. The method comprises  
 CC determining the time to clotting effected by a concentration of the  
 CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo  
 CC activated partial thromboplastin time (APTT) assay; calculating  
 CC prolongation of clotting effected by the isolated protein in each of  
 CC the PT and APTT assay, with respect to a baseline clotting value for  
 CC each assay, where prolongation of clotting is calculated as fold  
 CC elevation of clotting time relative to a baseline clotting value, where  
 CC a doubling of clotting time is deemed a two-fold elevation; and  
 CC calculating a PI to APTT prolongation ratio, where a ratio at least  
 CC one is indicative of factor VIIa/TF inhibitory activity. The method is  
 CC useful for determining if a protein has factor VIIa/TF inhibitory  
 CC activity.  
 CC  
 CC Sequence 91 AA;  
 S0  
 Query Match 100.0%; Score 486; DB 20; Length 91;  
 Host Local Similarity 100.0%; Pred. No. 66-39;  
 Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KATMGCGENFYVSTGSKETKTKKIVGVFFHFFHFNVPCTVWVHGVVPEGVFNK 50  
 Lp 8 KATMGCGENFYVSTGSKETKTKKIVGVFFHFFHFNVPCTVWVHGVVPEGVFNK 67  
 QY 61 DDKCVSAEDCELDMDPIYPTNRN 84  
 DB 68 ddkcvsaedcelmdmdfipyptnrn 91  
 RESULT 5  
 AAY30454  
 ID AAY30454 standard; Protein; 91 AA.  
 AC AAY30454;  
 XX  
 XX 15-NOV-1999 (first entry)  
 DE Nematode extracted anticoagulant protein *AcanNAPc2*.  
 XX  
 XX Nematode extracted anticoagulant protein; NAP; anticoagulant;  
 KW serine protease inhibitor; NAP domain; factor VIIa/TF.  
 XX  
 XX *Ancylostoma caninum*.  
 OS  
 XX







```

XX AC AAB15293;
XX
XX D1 19-DEC-2000 (first entry)
XX
XX DE A. ceylanicum nematode-extracted anticoagulant protein AacenAP42 #1.
XX
XX KM Nematode-extracted anticoagulant protein: AacenAP42; blood clotting;
XX canine hookworm; thrombosis; vaccine.
XX
XX OS Ancylostoma ceylanicum.
XX
XX PN US6087487-A.
XX
XX PD 11-JUL-2000.
XX
XX PF 12-FEB-1999; 9505-0249451.
XX
XX PR 17-OCT-1995; 95WO-0513231.
XX PR 17-APR-1997; 97US-0809455.
XX PR 18-OCT-1994; 94US-0326110.
XX PR 05-JUN-1995; 95US-0461965.
XX PR 05-JUN-1995; 95US-0465380.
XX PR 05-JUN-1995; 95US-0486397.
XX PR 05-JUN-1995; 95US-0486399.
XX
XX PA (CORV-) CORVAS INT INC.
XX
XX P1 Lauwereys MJ, Stanssens PHB, Jaspers LS, Ganssema's YGL, Moyle M;
XX Berquim PW, Messens JHT. Laboche YR, Vlasak GP;
XX
XX DP WPI: 2000-531359/48.
XX
XX PT New cDNA molecule encoding a protein having factor Xa inhibitory
XX activity for preventing and treating blood clotting disorders,
XX PT comprises nematode-extracted anticoagulant protein domains.
XX
XX PS Disclosure: Fig 11; 197pp; English.
XX
XX CC The present sequence is the Ancylostoma ceylanicum nematode-extracted
XX CC anticoagulant protein AacenAP42. Proteins of this kind have been shown to
XX CC be effective at preventing blood clotting without causing excessive
XX CC bleeding. The protein can be used in blood collection tubes to aid the
XX CC isolation of plasma from the blood, to prevent thrombosis which may be
XX CC linked to the rupture of an atherosclerotic plaque, acute myocardial
XX CC infarction, angina, thrombolytic therapy, percutaneous transluminal
XX CC coronary angioplasty, disseminated intravascular coagulopathy, infection,
XX CC cancer and septic shock, and to produce antibodies. In the latter
XX CC instance, the antibodies can be raised in order to detect infection by
XX CC nematodes or as diagnostic tests. The protein can also be used as a
XX CC vaccine against nematode parasites.
XX
XX S4 Sequence 82 AA;

```

Query Match 43.6%; Score 212; FB 21; Length 82;

Best Local Similarity 50.0%; Pred. No. 3, 1e-13;

Matches 38, Conservative 11; Mismatches 19; Indels 8; Gaps 3;

6 CGENEFKYSNGS-KEDCKKRYGVFEEDPEFNVFCLVWTHGLD-CVCEGFYKNUD 62

DB 4 cgsnefysdgnkqkqerckredyckxgde-----actshncezpgacvcdgfyrikkg 58

QY 63 KCVSAEDCELDNMDFI 78

DB 59 sevsdcdceydmndfi 74

```

RESULT 10
AAB15407
ID AAB15407 standard; Protein; 82 AA.
XX
XX AC AAB15407;

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XX AC AAB15407;
XX
XX D1 19-DEC-2000 (first entry)
XX
XX DE A. ceylanicum nematode-extracted anticoagulant protein AacenAP42 #1.
XX
XX KM Nematode-extracted anticoagulant protein: AacenAP42; blood clotting;
XX canine hookworm; thrombosis; vaccine.
XX
XX OS Ancylostoma ceylanicum.
XX
XX PN US6087487-A.
XX
XX PD 11-JUL-2000.
XX
XX PF 12-FEB-1999; 9505-0249451.
XX
XX PR 17-OCT-1995; 95WO-0513231.
XX PR 17-APR-1997; 97US-0809455.
XX PR 18-OCT-1994; 94US-0326110.
XX PR 05-JUN-1995; 95US-0461965.
XX PR 05-JUN-1995; 95US-0465380.
XX PR 05-JUN-1995; 95US-0486397.
XX PR 05-JUN-1995; 95US-0486399.
XX
XX PA (CORV-) CORVAS INT INC.
XX
XX P1 Lauwereys MJ, Stanssens PHB, Jaspers LS, Ganssema's YGL, Moyle M;
XX Berquim PW, Messens JHT, Laboche YR, Vlasak GP;
XX
XX DP WPI: 2000-531359/48.
XX
XX PT New cDNA molecule encoding a protein having factor Xa inhibitory
XX activity for preventing and treating blood clotting disorders,
XX PT comprises nematode-extracted anticoagulant protein domains.
XX
XX PS Disclosure: Fig 16; 197pp; English.
XX
XX CC The present sequence is the Ancylostoma ceylanicum nematode-extracted
XX CC anticoagulant protein AacenAP42. Proteins of this kind have been shown to
XX CC be effective at preventing blood clotting without causing excessive
XX CC bleeding. The protein can be used in blood collection tubes to aid the
XX CC isolation of plasma from the blood, to prevent thrombosis which may be
XX CC linked to the rupture of an atherosclerotic plaque, acute myocardial
XX CC infarction, angina, thrombolytic therapy, percutaneous transluminal
XX CC coronary angioplasty, disseminated intravascular coagulopathy, infection,
XX CC cancer and septic shock, and to produce antibodies. In the latter
XX CC instance, the antibodies can be raised in order to detect infection by
XX CC nematodes or as diagnostic tests. The protein can also be used as a
XX CC vaccine against nematode parasites.
XX
XX S0 Sequence 82 AA;

```

Query Match 43.6%; Score 212; DB 21; Length 82;

Best Local Similarity 50.0%; Pred. No. 3, 1e-13;

Matches 38, Conservative 11, Mismatches 19, Indels 8; Gaps 3;

6 CGENEFKYSNGS-KEDCKKRYGVFEEDPEFNVFCLVWTHGLD-CVCEGFYKNUD 62

DB 4 cgsnefysdgnkqkqerckredyckxgde-----actshncezpgacvcdgfyrikkg 58

QY 63 KCVSAEDCELDNMDFI 78

DB 59 sevsdcdceydmndfi 74

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RESULT 11
AAY30435
ID AAY30435 standard; Protein; 171 AA.
XX
XX AC AAY30435;
XX
XX DT 15-NOV-1999 (first entry)

```



Query Match 43.6%; Score 212; DB 17; Length 190;  
 Host Local Similarity 50.0%; Pred. No. 7.4e-13;  
 Matches 38; Conservative 11; Mismatches 19; Indels 8; Gaps 4;

6 CGENKRYISCGS-KETLKKKCYGVVEEEDPEPNVPTVWVHGN-CVCEGEPYANKDD 62  
 112 CGSNCRYSdGadkGcfrkncddGykade-----actshvcrpqacvcedgfyinkkg 166

63 KCVSAEKEELDNDPFI 78  
 167 scvsdceeydmndt 182

RESULT 13  
 AAY30384  
 ID AAY30384 standard; Protein: 190 AA.  
 AC AAY30384;  
 DT 15-NOV-1999 (first entry)  
 DE Nematode extracted anticoagulant protein AcenAP4.  
 KW Nematode extracted anticoagulant protein; NBP; anticoagulant;  
 KM serine protease inhibitor; NAP domain; factor VIIa/TF;  
 OS Ancylostoma ceylanicum.  
 PN US5955294-A.  
 PD 21-SEP-1999.  
 PP 19-APR-1996; 960S-0634641.  
 PR 19-APR-1996; 960S-0634641.  
 PR 18-OCT-1994; 94US-03326110.  
 PR 05-JUN-1995; 950S-0461965.  
 PR 05-JUN-1995; 950S-0465380.  
 PR 05-JUN-1995; 950S-0486397.  
 PR 05-JUN-1995; 950S-0486399.  
 PR 17-OCT-1995; 95WO-US13231.  
 XX  
 PA (CORV-) CORVAS INT INC.  
 PI Hartum FW, Ganssems YGL, Jespers JS, Laroché YR;  
 PI Lauwereys MJ, Messens JHL, Moyle M, Staessens PEH;  
 PI Vlasuk GP;  
 XX  
 DB WP1; 1999-539569/45.  
 DB N-PSDB; AAC10441.  
 XX  
 PT Screening an isolated protein for Nematode-extracted Anticoagulant  
 PT protein domains  
 PS Example 9; Fig 7A; 197pp; English.  
 XX  
 CC The present sequence represents a nematode extracted anticoagulant  
 CC protein (NBP). The protein has activity as an anticoagulant and/or serine  
 CC protease inhibitor. The protein contains at least one NAP domain which  
 CC has selective inhibitory activity for factor VIIa/TF. The specification  
 CC describes a method for screening an isolated protein at least one domain  
 CC for factor VIIa/TF selective inhibitory activity. The method comprises  
 CC determining the time to clotting effected by a concentration of the  
 CC isolated protein in an ex vivo prethrombin time (PT) assay and an ex vivo  
 CC activated partial thromboplastin time (aPTT) assay, calculating  
 CC prolongation of clotting effected by the isolated protein in each of  
 CC the PT and aPTT assay, with respect to a baseline clotting value for  
 CC each assay, where prolongation of clotting is calculated as fold  
 CC elevation of clotting time relative to a baseline clotting value, where  
 CC a doubling of clotting time is deemed a two-fold elevation; and  
 CC calculating a PT to aPTT prolongation ratio, where a ratio at least  
 CC one is indicative of factor VIIa/TF inhibitory activity. The method is  
 CC useful for determining if a protein has factor VIIa/TF inhibitory

CC activity.  
 XX  
 SQ Sequence 190 AA;

Query Match 43.6%; Score 212; DB 20; Length 190;  
 Host Local Similarity 50.0%; Pred. No. 7.4e-13;  
 Matches 38; Conservative 11; Mismatches 19; Indels 8; Gaps 4;

6 CGENKRYISCGS-KETLKKKCYGVVEEEDPEPNVPTVWVHGN-CVCEGEPYANKDD 62  
 112 CGSNCRYSdGadkGcfrkncddGykade-----actshvcrpqacvcedgfyinkkg 166

63 KCVSAEKEELDNDPFI 78  
 167 scvsdceeydmndt 182

RESULT 14  
 AAY30419  
 ID AAY30419 standard; Protein: 86 AA.  
 AC AAY30419;  
 DT 15-NOV-1999 (first entry)  
 DE Mature nematode extracted anticoagulant protein AcenAP4.  
 KW Nematode extracted anticoagulant protein; NBP; anticoagulant;  
 KM serine protease inhibitor; NAP domain; factor VIIa/TF;  
 OS Ancylostoma ceylanicum.  
 PN US5955294-A.  
 PD 21-SEP-1999.  
 PP 19-APR-1996; 960S-0634641.  
 PR 19-APR-1996; 960S-0634641.  
 PR 18-OCT-1994; 94US-03326110.  
 PR 05-JUN-1995; 950S-0461965.  
 PR 05-JUN-1995; 950S-0465380.  
 PR 05-JUN-1995; 950S-0486397.  
 PR 05-JUN-1995; 950S-0486399.  
 PR 17-OCT-1995; 95WO-US13231.  
 XX  
 PA (CORV-) CORVAS INT INC.  
 PI Hartum FW, Ganssems YGL, Jespers JS, Laroché YR;  
 PI Lauwereys MJ, Messens JHL, Moyle M, Staessens PEH;  
 PI Vlasuk GP;  
 XX  
 DB WP1; 1999-539569/45.  
 XX  
 PT Screening an isolated protein for Nematode extracted Anticoagulant  
 PT protein domains  
 PS Disclosure; Columns 131-134; 197pp; English.  
 XX  
 CC The present sequence represents a nematode extracted anticoagulant  
 CC protein (NBP). The protein has activity as an anticoagulant and/or serine  
 CC protease inhibitor. The protein contains at least one NAP domain which  
 CC has selective inhibitory activity for factor VIIa/TF. The specification  
 CC describes a method for screening an isolated protein at least one domain  
 CC for factor VIIa/TF selective inhibitory activity. The method comprises  
 CC determining the time to clotting effected by a concentration of the  
 CC isolated protein in an ex vivo prethrombin time (PT) assay and an ex vivo  
 CC activated partial thromboplastin time (aPTT) assay, calculating  
 CC prolongation of clotting effected by the isolated protein in each of  
 CC the PT and aPTT assay, with respect to a baseline clotting value for  
 CC each assay, where prolongation of clotting is calculated as fold  
 CC elevation of clotting time relative to a baseline clotting value, where























Query Match 19.48: Score 94.50 PR 1: length 4663.  
 Best Local Similarity 30.00: Pctd. No. 0.23  
 Matches 30: Conservative 11: Mismatches 24: Indels 35: Gaps 8:

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FT	DOMAIN	3113	3153	EGF-LIKE 11.
FT	DOMAIN	3154	3194	EGF-LIKE 12.
FT	DOMAIN	3241	3282	LDL-RECEPTOR CLASS B 30.
FT	DOMAIN	3284	3333	LDL-RECEPTOR CLASS B 31.
FT	DOMAIN	3335	3377	LDL-RECEPTOR CLASS B 32.
FT	DOMAIN	3379	3420	LDL-RECEPTOR CLASS B 33.
FT	DOMAIN	3421	3461	LDL-RECEPTOR CLASS B 34.
FT	DOMAIN	3462	3511	EGF-LIKE 13.
FT	DOMAIN	3512	3562	LDL-RECEPTOR CLASS A 35.
FT	DOMAIN	3563	3613	LDL-RECEPTOR CLASS A 36.
FT	DOMAIN	3614	3664	LDL-RECEPTOR CLASS A 37.
FT	DOMAIN	3665	3715	LDL-RECEPTOR CLASS A 38.
FT	DOMAIN	3716	3766	LDL-RECEPTOR CLASS A 39.
FT	DOMAIN	3767	3817	LDL-RECEPTOR CLASS A 40.
FT	DOMAIN	3818	3868	LDL-RECEPTOR CLASS A 41.
FT	DOMAIN	3869	3919	LDL-RECEPTOR CLASS A 42.
FT	DOMAIN	3920	3970	LDL-RECEPTOR CLASS A 43.
FT	DOMAIN	3971	4021	LDL-RECEPTOR CLASS A 44.
FT	DOMAIN	4022	4072	LDL-RECEPTOR CLASS A 45.
FT	DOMAIN	4073	4123	LDL-RECEPTOR CLASS A 46.
FT	DOMAIN	4124	4174	EGF-LIKE 14.
FT	DOMAIN	4175	4225	EGF-LIKE 15.
FT	DOMAIN	4226	4276	LDL-RECEPTOR CLASS B 35.
FT	DOMAIN	4277	4327	LDL-RECEPTOR CLASS B 36.
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FT	DOMAIN	4379	4429	EGF-LIKE 17.
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FT	DOMAIN	4532	4582	SH3-BINDING (POTENTIAL).
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FT				





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FT	DISULFID	1423	1435	BY SIMILARITY
FT	DISULFID	1441	1451	BY SIMILARITY
FT	DISULFID	1447	1450	BY SIMILARITY
FT	DISULFID	1462	1475	BY SIMILARITY
FT	DISULFID	1751	1760	BY SIMILARITY
FT	DISULFID	1756	1770	BY SIMILARITY
FT	DISULFID	1772	1785	BY SIMILARITY
FT	DISULFID	2084	2095	BY SIMILARITY
FT	DISULFID	2091	2105	BY SIMILARITY
FT	DISULFID	2107	2119	BY SIMILARITY
FT	DISULFID	2400	2415	BY SIMILARITY
FT	DISULFID	2411	2426	BY SIMILARITY
FT	DISULFID	2428	2438	BY SIMILARITY
FT	DISULFID	2732	2743	BY SIMILARITY
FT	DISULFID	2739	2759	BY SIMILARITY
FT	DISULFID	2761	2779	BY SIMILARITY
FT	DISULFID	2792	2805	BY SIMILARITY
FT	DISULFID	2805	2818	BY SIMILARITY
FT	DISULFID	2812	2829	BY SIMILARITY
FT	DISULFID	2824	2846	BY SIMILARITY
FT	DISULFID	2841	2859	BY SIMILARITY
FT	DISULFID	2853	2864	BY SIMILARITY
FT	DISULFID	2874	2886	BY SIMILARITY
FT	DISULFID	2881	2899	BY SIMILARITY
FT	DISULFID	2893	2912	BY SIMILARITY
FT	DISULFID	2919	2942	BY SIMILARITY

Query Match	19.0%	Score 92.5	PR 1	Length 4758
Best Local Similarity	25.0%	Prod No 0	31	
Matches	28	Conservative	11	Mismatches 32
				Indels 4

[illegible]

	RESULT	5
	VWF_CANFA	
ID	VWF CANFA	STANDARD:
	0.00007	EFT:
	0.00007	2813 AA
	0.00007	0.00004

```

PT      01-NOV-1997 (Rel 35, Created)
DT      01-OCT-2008 (Rel 40, 1st sequence update)
DT      01-OCT-2008 (Rel 40, 1st annotation update)
DE      ON WILHELM BRAND FACTOR PROTEIN (WBF)
CN      F8WF OR WBF
OS      Canis familiaris (dog)
OC      Eukaryota, Mollusca, Chordata, Craniata, Vertebrata, Euteleostomi,
OC      Mammalia, Eutheria: Carnivora: Fissipedia: Canidae: Canis.
OX      NCBI_Taxid=9615;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Stroy S I, Shinya H, Newman P J, Holzhauer J, Mohammad T H,
RA      Johnson G S,
RL      Submitted (AUG-1996) to the EMBL/Genbank/JGI databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Montgomery R P, Fabs S, Montgomery M W,
RL      Submitted (AUG-1996) to the EMBL/Genbank/JGI databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RA      Vendi P T, Li T, Yambaslan-Durhan V, Brown G T, Stahl W P,
RT      "Complete sequence of the structural gene for canine von Willebrand
RT      factor and identification of a mutation causing Scottish terrier von
RT      Willebrand's disease".
RL      Submitted (OCT-1998) to the EMBL/Genbank/JGI databases.
RN      [4]
RP      SEQUENCE OF 1234-1664 FROM N.A.
RT      TISSUE-Blood;

```

PA	Martinsen T, Christoffersen P A., Kruut P A., Møller-Pedersen P F.: "The value you willibidand factor gene: sequence and expression of a region encoding the glycoprotein Ib/IX binding domain."
R1	SUBMITTED (JAN-1994) TO THE EMBL/GENBANK/DBJ DATABASES.
RL	-1 FUNCTION: IMPORTANT IN THE MAINTENANCE OF HEMOSTASIS. IT PARTICIPATES IN PLATELET-VESSEL WALL INTERACTIONS BY FORMING A NONVALENT COMPLEX WITH CAVITATION FACTOR VIT AT THE SITE OF VASCULAR INJURY. (BY SIMILARITY).
CC	-1 SERINITY: MULTIMERIC (BY SIMILARITY).
CC	-1 TISSUE SPECIFICITY: BLOOD.
CC	-1 PM: ALL CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN OR INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).
CC	-1 SIMILARITY: CONTAINS 3 VWFA DOMAINS.
CC	-1 SIMILARITY: CONTAINS 3 VWFC DOMAINS.
CC	-1 SIMILARITY: CONTAINS 4 VWFD DOMAINS.
CC	-1 SIMILARITY: SOME TO SICKLE CELL HEMOGLOBIN.
CC	-1 This SwissProt entry is copy-right. It is provided through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. usage by and for commercial purposes requires a license agreement (See <a href="http://www.isdb.ch/info/entry.html">http://www.isdb.ch/info/entry.html</a> or send an email to <a href="mailto:license@isdb.ch">license@isdb.ch</a> )
CC	EMBL L76227, AAC05149.1; -
DE	EMBL L16903, AAA30903.1; -
DR	EMBL AF094154, AAP04419.1; -
DR	EMBL U06248, AAU93766.1; -
DR	HSSP, P04275; IATZ.
DR	InterPro: IPRO00359; -
IR	In-CRTP, IPRO01007; -
DR	InterPro: IPRO01846; -
IR	In-CRTP, IPRO01035; -
DR	InterPro: IPRO02919; -
DR	Ffam: PF00607; Cys_Knot_1.
DR	Ffam: PF01826; TL; 4.
IR	Ffam: PF00992; VWB; 3.
DR	Ffam: PF00993; VWG; 3.
DR	Ffam: PF00994; Wvd; 4.
DR	PRINTS: PRO0453; VWPADOMAIN
DR	PROSITE: PS01185; CTCK_1; 1
DR	PROSITE: PS01250; CTCK_2; 1.
DR	PROSITE: PS02394; VWFA; 3.
DR	PROSITE: PS01208; VWFC; 3.
FW	Ricin-B agglutinin. Platelet-derived plasma: Endothelial cells; Fibroblasts; Cell adhesion; Signal.
KW	SIGNAL.
FT	PROPEP 1 22
FT	PROPEP 23 763
FT	CHAIN 764 2813
FT	DOMAIN 35 179
FT	DOMAIN 488 541
FT	DOMAIN 764 787
FT	DOMAIN 788 833
FT	DOMAIN 826 853
FT	DOMAIN 867 1013
FT	DOMAIN 1277 1453
FT	DOMAIN 1498 1665
FT	DOMAIN 1691 1871
FT	DOMAIN 1950 2102
FT	DOMAIN 2216 2261
FT	DOMAIN 2326 2495
FT	DOMAIN 2429 2495
FT	DOMAIN 2580 2650
FT	DOMAIN 2724 2812
FT	SITE 531 533
FT	SITE 684 760
FT	SITE 767 808
FT	DISULFID 776 804
FT	DISULFID 810 821
FT	DISULFID 867 996
FT	DISULFID 867 996

[illegible][illegible]

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30 SEQUENCE 115 AA: 12579 MW: 42265ADAEED32294D1ED2543;
Query Match 17.9% Score 87; DB 1; Length 115;
Post Local Similarity 31.0%; Pred No 0.042;
Matches 22; Conserved 8; Mismatches 23; Gaps 12; Gaps 4
CY 4 MOCIFNEKYSSTKSRKQKQYVWEVFHDEHPHVPPIVWVQVQVCEDEEYKFKD 62
DB 32 VFTANLTQFT PAVTFEITLYSD-----NAPVMAAPVAPVLYINERIP 80
UY 63 KVSAPDELD 73
UY 11 11 1
DB 81 ACVLSPDCKD 91
DB 11 11 1
RESULT 7
LBP2_HUMAN STANDARD; PRT; 4655 AA.
11 LBP2_HUMAN
AC P98164; 000711; Q16215;
DI 01-OCT-1996 (Rel. 34; Created)
DI 15-DEC-1998 (Rel. 37; Last sequence update)
DI 01-OCT-2000 (Rel. 40; Last annotation update)
DE LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 (MIFALIN)
DE (Glycoprotein 330)
DE LBP2.
DE Homo sapiens (human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Primates; Catarrhini; Hominoidea; Homo;
OX NCBI_TaxID=9606;
RN 111
RP SEQUENCE FROM N A
RC TISSUE=Kidney;
RA MEDLINE=66305376; PubMed 8706697;
RA Hjaelm G., Murray F., Cromley G., Harazin M., Lindgren S., Argaves W.,
RA Ek R., Larsson M., Juhlin C., Hellman P., Davis H., Akerstrom G.,
RA Kask L., Morse B.;
RA "Cloning and sequencing of human gp330, a (9+2)-binding receptor
R1 with potential intracellular signaling properties."
R1 Eur. J. Biochem. 239:132-137(1996).
RN 121
RP SEQUENCE OF 2705-4453 FROM N.A.
RC TISSUE=Kidney;
RA Knudsk C., Argaves W.S.;
RA Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
RN 131
RP SEQUENCE OF 3433-4453 FROM N A
RC TISSUE=Kidney;
RA MEDLINE=95045337; PubMed-759375;
RA Korenberg J.R., Argaves K.M., Chen X.N., Tran H.;
RA Strickland D.R., Argaves W.S.;
RA "Chromosomal localization of human genes for the LDL receptor family
R1 member 2 (LDLR-2) (1412) and its associated protein (LAP2)
R1 (LRPAP1)."
R1 Genomics 22:88-93(1994).
RN 141
RP SEQUENCE OF 4139-4406 FROM N.A.
RC MEDLINE=94244704; PubMed 8187828;
RA Lindgren S., Hjaelm G., Hellman P., Ek R., Juhlin C., Pasted J.,
RA Kareskog L., Akerstrom G., Park L.;
RA "A protein involved in calcium sensing of the human parathyroid and
R1 placental cytotrophoblast cells belongs to the LDL receptor protein
R1 superfamily."
R1 Exp. Cell Res. 212:344-350(1994).
RN 151
RP FUNCTION.
RP MEDLINE=95286588; PubMed 776901;
RA Komatsu M., Jonkheva F.B., Stenstrom S., Hultberg A.K.,
RA Brower R.H., Strickland D.K., Argaves W.S.;
RA "Identification of glycoprotein 330 as an endocytic receptor for
R1 apolipoprotein 17/18/19."
R1 J. Biol. Chem. 270:13070-13075(1995).
R1 1- FUNCTION: BINDS SPECIFICALLY CLUSTERIN WITH HIGH AFFINITY. NOT

```

CC	ALSTILANS IN COMMON WITH OTHER FAMILY MEMBERS: PLASMINOGEN,
CC	EXTRACELLULAR MATRIX COMPONENTS, PLASMINOGEN ACTIVATOR-PLASMINOGEN
CC	ACTIVATOR INHIBITOR TYPE 1 COMPLEX, APOLIPOPROTEIN E-ENRICHED
CC	BETA-VLDL, LIPOPROTEIN LIPASE, LACTOFERRIN AND CALCIUM.
CC	-1- FUNCTION: PROPEPTIDE-MEDIATED HYDRAZYDE OF POLYPHOSPHATE DRUGS SUCH AS
CC	ALICLININ, AMINOCAPROATES AND FOLYMERIN B (4% SIMILARITY).
CC	-1- FUNCTION: MAY PARTICIPATE IN REGULATION OF PARATHYROID-HORMONE AND
CC	PABA-1,2-DIOL-1-OXIMINE-RELATED PROTEIN RELEASE.
CC	-1- SUBUNIT: FORMS A MULTIMERIC COMPLEX TOGETHER WITH A RECEPTOR-
CC	ASSOCIABLE PROTEIN (PAR).
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	-1- TISSUE SPECIFICITY: ABSORPTIVE EPITHELIA, INCLUDING RENAL
CC	PROXIMAL TUBULES.
CC	-1- SIMILARITY: CONTAINS 36 LDL-RECEPTOR CLASS A DOMAINS.
CC	-1- SIMILARITY: CONTAINS 47 LDL-RECEPTOR CLASS B DOMAINS.
CC	-1- SIMILARITY: CONTAINS 17 EGF-LIKE DOMAINS.
CC	-1- SIMILARITY: CONTAINS 4 SH3-BINDING DOMAINS.
CC	-1- SIMILARITY: CONTAINS 1 SH2-BINDING DOMAIN.
CC	-----
CC	This SWISS-Prot entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL institution.
CC	The European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed, copied by and for commercial
CC	purposes or used as a basis for patenting (see http://www.isdb.ch).
CC	-----
CC	PMID: 933837; AAA1649.1;
CC	PMID: 904441; AA02289.1;
CC	PMID: S73145; AA02025.1;
CC	HSSP: P01130; JALI.
CC	MIM: 600073;
DR	InterPro: IPRO00033;
DR	InterPro: IPRO00152;
DR	InterPro: IPRO00561;
DR	InterPro: IPRO01881;
DR	InterPro: IPRO02172;
DR	PIfam: PF00098; Pfam: 13.
DR	PIfam: PF00057; Idl_recept_a: 36.
DR	PIfam: PF00058; Idl_recept_b: 37.
DR	PRINTS: PR00261; LDLRECEPT.
DR	PROSITE: PS00010; ASX_HYDROXYL_4.
DR	PROSITE: PS00032; EGF_1; 1.
DR	PROSITE: PS01186; EGF_2; 9.
DR	PROSITE: PS01187; EGF_CA; 3.
DR	PROSITE: PS01209; LDLR_A_1; 31.
DR	PROSITE: PS00068; LDLR_A_2; 36.
KW	Glycoprotein, Integral, Folded filts, Trans-membrane,
KW	Receptor, EGF-like domain, Signal, Polymorphism.
FT	SIGNAL 1 25
FT	CMAIN 26 4555
FT	-----
FT	1-MAIN 25 4473
FT	TRANSMEM 4424 4446
FT	DOMAIN 4447 4655
FT	DOMAIN 26 64
FT	DOMAIN 65 105
FT	DOMAIN 106 144
FT	DOMAIN 145 181
FT	DOMAIN 182 219
FT	DOMAIN 220 258
FT	DOMAIN 264 308
FT	DOMAIN 309 347
FT	DOMAIN 348 386
FT	DOMAIN 436 477
FT	DOMAIN 479 520
FT	DOMAIN 522 567
FT	DOMAIN 569 613
FT	DOMAIN 613 653
FT	DOMAIN 654 705
FT	DOMAIN 753 794
FT	DOMAIN 796 846
FT	DOMAIN 848 880
FT	-----
FT	LOW-INTENSITY LIPOPROTEIN RECEPTOR-RELATED
FT	PROTEIN 2.
FT	EXTRACELLULAR (POTENTIAL).
FT	POTENTIAL.
FT	CYTOSOLASMIC (POTENTIAL).
FT	LDL-RECEPTOR CLASS A 1.
FT	LDL-RECEPTOR CLASS A 2.
FT	LDL-RECEPTOR CLASS A 3.
FT	LDL-RECEPTOR CLASS A 4.
FT	LDL-RECEPTOR CLASS A 5.
FT	LDL-RECEPTOR CLASS A 6.
FT	LDL-RECEPTOR CLASS A 7.
FT	EGF-LIKE 1.
FT	EGF-LIKE 2.
FT	LDL-RECEPTOR CLASS B 1.
FT	LDL-RECEPTOR CLASS B 2.
FT	LDL-RECEPTOR CLASS B 3.
FT	LDL-RECEPTOR CLASS B 4.
FT	LDL-RECEPTOR CLASS B 5.
FT	EGF-LIKE 3.
FT	LDL-RECEPTOR CLASS B 6.
FT	LDL-RECEPTOR CLASS B 7.
FT	LDL-RECEPTOR CLASS B 8.

FT	DOMAIN	982	924	LDL-RECEPTOR CLASS B 9.
FT	DOMAIN	970	1014	EGF-LIKE 4.
FT	DOMAIN	1024	1062	LDL-RECEPTOR CLASS A 8.
FT	DOMAIN	1065	1103	LDL-RECEPTOR CLASS A 9.
FT	DOMAIN	1137	1145	LDL-RECEPTOR CLASS A 10.
FT	DOMAIN	1147	1185	LDL-RECEPTOR CLASS A 11.
FT	DOMAIN	1186	1224	LDL-RECEPTOR CLASS A 12.
FT	DOMAIN	1228	1268	LDL-RECEPTOR CLASS A 13.
FT	DOMAIN	1269	1307	LDL-RECEPTOR CLASS A 14.
FT	DOMAIN	1310	1350	LDL-RECEPTOR CLASS A 15.
FT	DOMAIN	1349	1389	EGF-LIKE 5.
FT	DOMAIN	1390	1429	EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	1478	1519	LDL-RECEPTOR CLASS B 10.
FT	DOMAIN	1521	1562	LDL-RECEPTOR CLASS B 11.
FT	DOMAIN	1566	1608	LDL-RECEPTOR CLASS B 12.
FT	DOMAIN	1610	1653	LDL-RECEPTOR CLASS B 13.
FT	DOMAIN	1655	1695	LDL-RECEPTOR CLASS B 14.
FT	DOMAIN	1700	1741	EGF-LIKE 7.
FT	DOMAIN	1790	1831	LDL-RECEPTOR CLASS B 15.
FT	DOMAIN	1843	1881	LDL-RECEPTOR CLASS B 16.
FT	DOMAIN	1883	1929	LDL-RECEPTOR CLASS B 17.
FT	DOMAIN	1941	1971	LDL-RECEPTOR CLASS B 18.
FT	DOMAIN	1972	2012	LDL-RECEPTOR CLASS B 19.
FT	DOMAIN	2018	2059	EGF-LIKE 8.
FT	DOMAIN	2137	2155	LDL-RECEPTOR CLASS B 20.
FT	DOMAIN	2157	2200	LDL-RECEPTOR CLASS B 21.
FT	DOMAIN	2292	2344	LDL-RECEPTOR CLASS B 22.
FT	DOMAIN	2246	2288	LDL-RECEPTOR CLASS B 23.
FT	DOMAIN	2290	2331	LDL-RECEPTOR CLASS B 24.
FT	DOMAIN	2342	2383	EGF-LIKE 9.
FT	DOMAIN	2431	2476	LDL-RECEPTOR CLASS B 25.
FT	DOMAIN	2478	2517	LDL-RECEPTOR CLASS B 26.
FT	DOMAIN	2519	2561	LDL-RECEPTOR CLASS B 27.
FT	DOMAIN	2564	2603	LDL-RECEPTOR CLASS B 28.
FT	DOMAIN	2604	2646	LDL-RECEPTOR CLASS B 29.
FT	DOMAIN	2651	2693	EGF-LIKE 10.
FT	DOMAIN	2698	2738	LDL-RECEPTOR CLASS A 16.
FT	DOMAIN	2739	2777	LDL-RECEPTOR CLASS A 17.
FT	DOMAIN	2778	2819	LDL-RECEPTOR CLASS A 18.
FT	DOMAIN	2820	2861	LDL-RECEPTOR CLASS A 19.
FT	DOMAIN	2862	2901	LDL-RECEPTOR CLASS A 20.
FT	DOMAIN	2904	2945	LDL-RECEPTOR CLASS A 21.
FT	DOMAIN	2946	2990	LDL-RECEPTOR CLASS A 22.
FT	DOMAIN	2991	3029	LDL-RECEPTOR CLASS A 23.
FT	DOMAIN	3030	3070	LDL-RECEPTOR CLASS A 24.
FT	DOMAIN	3073	3110	LDL-RECEPTOR CLASS A 25.
FT	DOMAIN	3111	3151	EGF-LIKE 11.
FT	DOMAIN	3152	3192	EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	3239	3280	LDL-RECEPTOR CLASS B 30.
FT	DOMAIN	3282	3331	LDL-RECEPTOR CLASS B 31.
FT	DOMAIN	3333	3375	LDL-RECEPTOR CLASS B 32.
FT	DOMAIN	3377	3418	LDL-RECEPTOR CLASS B 33.
FT	DOMAIN	3419	3459	LDL-RECEPTOR CLASS B 34.
FT	DOMAIN	3465	3509	EGF-LIKE 13.
FT	DOMAIN	3510	3550	LDL-RECEPTOR CLASS A 26.
FT	DOMAIN	3551	3591	LDL-RECEPTOR CLASS A 27.
FT	DOMAIN	3592	3632	LDL-RECEPTOR CLASS A 28.
FT	DOMAIN	3633	3673	LDL-RECEPTOR CLASS A 29.
FT	DOMAIN	3676	3716	LDL-RECEPTOR CLASS A 30.
FT	DOMAIN	3717	3756	LDL-RECEPTOR CLASS A 31.
FT	DOMAIN	3757	3795	LDL-RECEPTOR CLASS A 32.
FT	DOMAIN	3796	3834	LDL-RECEPTOR CLASS A 33.
FT	DOMAIN	3840	3880	LDL-RECEPTOR CLASS A 34.
FT	DOMAIN	3881	3922	LDL-RECEPTOR CLASS A 35.
FT	DOMAIN	3926	3964	LDL-RECEPTOR CLASS A 36.
FT	DOMAIN	3968	4006	EGF-LIKE 14.
FT	DOMAIN	4007	4048	EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	4154	4195	LDL-RECEPTOR CLASS B 35.
FT	DOMAIN	4197	4239	LDL-RECEPTOR CLASS B 36.
FT	DOMAIN	4242	4282	LDL-RECEPTOR CLASS B 37.
FT	DOMAIN	4330	4368	EGF-LIKE 16.
FT	DOMAIN	4377	4411	EGF-LIKE 17.

[illegible]

DE (VITELLOGENIN RECEPTOR) (VTG RECEPTOR).  
 GN VITR OR VTGR.  
 OS Gallus gallus (Chicken).  
 OC Phalaropus lobatus, Chordata: Vertebrata: Eupolystomi:  
 OC Archosauria: Aves: Neognathae: Galliformes: Phasianidae: Phasianinae:  
 OC Gallus.  
 CX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 PC STEIN-WHITE LEBROHN: TISSUE-EXTRACT;  
 RX MEDLINE=95045409; PubMed=7957081;  
 RA Buto H., Hermann M., Nadelmann M.O., Jacobsen L., Steward S.,  
 RA Nijmpt J., Yamamoto T., Schneider W.J.;  
 RT "Chronic overexpression of a single ligand-binding repeat  
 member of the LDL receptor family";  
 RL EMBO J. 13:5165-5175(1994).  
 KN [2]  
 RP SEQUENCE OF 510-518: 546-554 AND 819-827.  
 PC STEIN-WHITE LEBROHN: TISSUE-POLICLE MEMBRANE;  
 RX MEDLINE=9201638; PubMed=1655760;  
 RA Barber D.L., Sanders E.J., Abersold R., Schneider W.J.;  
 RT "The receptor for yolk lipoprotein deposition in the chicken ovary";  
 RL J Biol Chem 267:18911-18919(1992).  
 CC -1- FUNCTION: KININS WITH ANO-VIS TRANSPORTS THEM INTO CELLS BY  
 CC ENDOCYTOSIS. IN ORDER TO BE INTERNALIZED, THE RECEPTOR LIGAND  
 CC COMPLEXES MUST FIRST CLUSTER INTO CLATHRIN-COATED PITS.  
 CC -1- SUBCELLULAR LOCATION: TYPE: MEMBRANE PROTEIN  
 CC -1- TISSUE SPECIFICITY: ADHUCANT IN OVARY; MUCH LESS IN HEART AND  
 CC SKELETAL MUSCLE.  
 CC -1- SIMILARITY: CONTAINS 8 LDL-RECEPTOR CLASS A DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 6 LDL-RECEPTOR CLASS B DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC modified and this statement is not removed. Usage by and for commercial  
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FT DOMAIN 374 413 BOE-LIKE 1, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 414 453 BOE-LIKE 2, CALCIUM-BINDING (POTENTIAL).  
 FT REPEAT 457 498 LDL-RECEPTOR CLASS B 1.  
 FT REPEAT 499 544 LDL-RECEPTOR CLASS B 2.  
 FT REPEAT 545 587 LDL-RECEPTOR CLASS B 3.  
 FT REPEAT 588 631 LDL-RECEPTOR CLASS B 4.  
 FT REPEAT 632 674 LDL-RECEPTOR CLASS B 5.  
 FT REPEAT 675 716 LDL-RECEPTOR CLASS B 6.  
 FT REPEAT 717 759 EGF-LIKE 3.  
 FT DOMAIN 760 827 ENDOCYTOSIS SIGNAL (POTENTIAL).  
 FT DISULFID 828 837 BY SIMILARITY.  
 FT DISULFID 838 855 BY SIMILARITY.  
 FT DISULFID 856 873 BY SIMILARITY.  
 FT DISULFID 874 891 BY SIMILARITY.  
 FT DISULFID 892 909 BY SIMILARITY.  
 FT DISULFID 910 927 BY SIMILARITY.  
 FT DISULFID 928 945 BY SIMILARITY.  
 FT DISULFID 946 963 BY SIMILARITY.  
 FT DISULFID 964 981 BY SIMILARITY.  
 FT DISULFID 982 999 BY SIMILARITY.  
 FT DISULFID 1000 1017 BY SIMILARITY.  
 FT DISULFID 1018 1035 BY SIMILARITY.  
 FT DISULFID 1036 1053 BY SIMILARITY.  
 FT DISULFID 1054 1071 BY SIMILARITY.  
 FT DISULFID 1072 1089 BY SIMILARITY.  
 FT DISULFID 1090 1107 BY SIMILARITY.  
 FT DISULFID 1108 1125 BY SIMILARITY.  
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 FT DISULFID 1162 1179 BY SIMILARITY.  
 FT DISULFID 1180 1197 BY SIMILARITY.  
 FT DISULFID 1198 1215 BY SIMILARITY.  
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 FT DISULFID 1234 1251 BY SIMILARITY.  
 FT DISULFID 1252 1269 BY SIMILARITY.  
 FT DISULFID 1270 1287 BY SIMILARITY.  
 FT DISULFID 1288 1305 BY SIMILARITY.  
 FT DISULFID 1306 1323 BY SIMILARITY.  
 FT DISULFID 1324 1341 BY SIMILARITY.  
 FT DISULFID 1342 1359 BY SIMILARITY.  
 FT DISULFID 1360 1377 BY SIMILARITY.  
 FT DISULFID 1378 1395 BY SIMILARITY.  
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 FT DISULFID 1504 1521 BY SIMILARITY.  
 FT DISULFID 1522 1539 BY SIMILARITY.  
 FT DISULFID 1540 1557 BY SIMILARITY.  
 FT DISULFID 1558 1575 BY SIMILARITY.  
 FT DISULFID 1576 1593 BY SIMILARITY.  
 FT DISULFID 1594 1611 BY SIMILARITY.  
 FT DISULFID 1612 1629 BY SIMILARITY.  
 FT DISULFID 1630 1647 BY SIMILARITY.  
 FT DISULFID 1648 1665 BY SIMILARITY.  
 FT DISULFID 1666 1683 BY SIMILARITY.  
 FT DISULFID 1684 1701 BY SIMILARITY.  
 FT DISULFID 1702 1719 BY SIMILARITY.  
 FT DISULFID 1720 1737 BY SIMILARITY.  
 FT DISULFID 1738 1755 BY SIMILARITY.  
 FT DISULFID 1756 1773 BY SIMILARITY.  
 FT CARBOHYD 1774 1779 N-LINKED (GLCNAC).  
 FT CARBOHYD 1780 1785 N-LINKED (GLCNAC).  
 FT SIGNATURE 855 AA; 94704 MW; 367280748P:AA245 CR654;  
 Query Match 17.6%; Score 85.5; DB 1; Length 863;  
 Best Local Similarity 33.3%; Pred. No. 0.3;  
 Matches 25; Conservative 9; Mismatches 36; Indels 5; Gaps 4;  
 27 4 MDCENENYEDSGSEKELKKKATLVEEELDEPNPCVVPVCHGVVTPRFRPNKD 61  
 28 255 VCGSTSEV-CQGSFPCIRKRWKPTDTPKQSPINPSPPTPPVQPPCEFTGNC 312  
 29 62 DKCVASPCPELDNMD 76  
 30 313 KQTNVVRK-LEGTD 326  
 RESULT 10  
 LDDR\_HUMAN STANDARD; PRT; 873 AA.  
 AC P69155;  
 DT 01-OCT-1996 (Ref. 34, Created)  
 DT 01-OCT-1996 (Ref. 34, Last sequence update)  
 DT 01-OCT-2000 (Ref. 40, Last annotation update)  
 DE VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR).  
 GN VLDLR.  
 OS Homo sapiens (human).  
 OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:  
 OC Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.

00 NBI\_FaxID 9606;  
 01 [1]  
 02 SEQUENCE FROM N.A.  
 03 TISSUE: Skeletal muscle;  
 04 MEDLINE 9417478; PubMed 812815;  
 05 Kato T, Miki M, Fard M, Britz D, Jackson C L, Patterson D,  
 06 Strauss J.F.;  
 07 "Cloning of a cDNA encoding a putative human very low density  
 08 lipoprotein/apoE receptor and assignment of the gene to  
 09 chromosome 9p11-p23";  
 10 Genet. Cell Mol. Genet. 19:557-569(1993).  
 11 [2]  
 12 SEQUENCE FROM N.A.  
 13 TISSUE: Heart;  
 14 MEDLINE 9434846; PubMed 8069294;  
 15 Webb J.C., Patel D.D., Jones M.D., Knight R.L., Soutar A.K.;  
 16 "Characterization and tissue-specific expression of the human very  
 17 low density lipoprotein (VLDL) receptor mRNA";  
 18 Hum. Mol. Genet. 3:531-537(1994).  
 19 [3]  
 20 SEQUENCE FROM N.A.  
 21 MEDLINE 9412475; PubMed 8294473;  
 22 Sakai I, Hashino A, Takahashi S., Miura Y., Ishii H., Suzuki H.,  
 23 Kawachiya Y., Yamamoto T.;  
 24 "Structure, chromosome location, and expression of the human very low  
 25 density lipoprotein receptor gene";  
 26 J. Biol. Chem. 269:2173-2182(1994).  
 27 [4]  
 28 SEQUENCE FROM N.A.  
 29 TISSUE: Heart;  
 30 MEDLINE 9429216; PubMed 8020981;  
 31 Oka K., Izumi K.W., Sullivan M., Lindsay E., Baldwin A., Chan L.;  
 32 "Human very low density lipoprotein receptor complementary DNA and  
 33 deduced amino acid sequence and localization of its gene (VLDLR) to  
 34 chromosome band 9p24 by fluorescence in situ hybridization";  
 35 Genomics 20:298-300(1994).  
 36 [5]  
 37 FUNCTION: BINDS VLDL AND TRANSPORTS IT INTO CELLS BY ENDOCYTOSIS.  
 38 IN ORDER TO BE INTERNALIZED, THE RECEPTOR-LIGAND COMPLEXES MUST  
 39 FIRST CLUSTER INTO CLATHRIN-COATED PITS (BY SIMILARITY).  
 40 TISSUE SPECIFICITY: TYPE I MEMBRANE PROTEIN.  
 41 SIMILARITY: ABUNDANT IN HEART AND SKELETAL MUSCLE; ALSO  
 42 Ovary and kidney; NOT IN LIVER.  
 43 SIMILARITY: CONTAINS 8 LDL-RECEPTOR CLASS A DOMAINS.  
 44 SIMILARITY: CONTAINS 6 LDL-RECEPTOR CLASS B DOMAINS.  
 45 SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.  
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 47 This Swiss-Prot entry is copyright. It is produced through a collaboration  
 48 between the Swiss Institute of Bioinformatics and the EMBL outstation  
 49 at the European Bioinformatics Institute. There are no restrictions on its  
 50 use by non-profit institutions as long as its content is in no way  
 51 modified and this statement is not removed, usage by and for commercial  
 52 entities requires a license agreement (See <http://www.isb.slb.ch/announcements>  
 53 or send an email to [license@isb.slb.ch](mailto:license@isb.slb.ch)).  
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 56 EMBL: L20470; AAA53684.1; -;  
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 393 EMBL: D16432; BAA03969.1; JOINED.  
 394 EMBL: D16432; BAA03969.1; JOINED.  
 395 EMBL: D16432; BAA03969.1; JOINED.  
 396 EMBL: D16432; BAA03969.1; JOINED.  
 397 EMBL: D16432; BAA03969.1; JOINED.  
 398 EMBL: D16432; BAA03969.1; JOINED.  
 399 EMBL: D16432; BAA03969.1; JOINED.  
 400 EMBL: D16432; BAA03969.1; JOINED.  
 401 EMBL: D16432; BAA03969.1; JOINED.  
 402 EMBL: D16432; BAA0



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CC	TISSUE
CC	-1- SIMILARITY: CONTAINS 8 LDL-RECEPTOR CLASS A DOMAINS.
CC	-1- SIMILARITY: CONTAINS 6 LDL-RECEPTOR CLASSES B DOMAINS.
CC	-1- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
CC	This Swiss-Prot entry is copyright . It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL collaboration at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/aboutus/ezyor-send-an-email-to-license@isb-sib.ch">http://www.isb-sib.ch/aboutus/ezyor-send-an-email-to-license@isb-sib.ch</a> ).
CC	EMBL: D11100; -1 NOT_ANNOTATED_CDS.
DR	PIR: AA6286; GPRVH.
DR	HSSP: P01130; IAUJ.
DR	InterPro: IFRO00933; -1
DR	InterPro: IPRO00152; -1
DR	InterPro: IPRO00561; -1
DR	InterPro: IPRO01881; -1
DR	InterPro: IPRO02172; -1
DR	Pfam: PF000057; LDL_recept_b; 8.
DR	Pfam: PF000058; LDL_recept_b; 5.
DR	PRINTS: PR00261; LDLRECEPTOR.
DR	PROSITE: PS00910; ASX_HYDPOXYL; 2.
DR	PROSITE: PS00022; EGF_1; FALSE_NEG.
DR	PROSITE: PS01146; EGF_2; 3.
DR	PROSITE: PS01187; EGF_CA; 1.
DR	PROSITE: PS01209; LDLPA_1; 8.
DR	PROSITE: PS00958; LDLPA_2; 8.
KM	Glycoprotein YLDL cholesterol metabolism; lipid transport;
KM	Endocytosis; Coated pits; Transmembrane Receptor; Signal;
KM	EGF-like domain; Peptid-
FT	SIGNAL 1 27 POTENTIAL.
FT	CHAIN 28 873 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR.
FT	DOMAIN 28 797 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 798 819 POTENTIAL.
FT	DOMAIN 820 873 CYTOSOLIC (POTENTIAL).
FT	PT DOMAIN 31 69 LDL-RECEPTOR CLASS A 1.
FT	PT DOMAIN 70 119 LDL-RECEPTOR CLASS A 2.
FT	PT DOMAIN 111 151 LDL-RECEPTOR CLASS A 3.
FT	PT DOMAIN 152 190 LDL-RECEPTOR CLASS A 4.
FT	PT DOMAIN 191 231 LDL-RECEPTOR CLASS A 5.
FT	PT DOMAIN 237 275 LDL-RECEPTOR CLASS A 6.
FT	PT DOMAIN 276 314 LDL-RECEPTOR CLASS A 7.
FT	PT DOMAIN 316 355 LDL-RECEPTOR CLASS A 8.
FT	PT DOMAIN 356 395 EGF-LIKE 1.
FT	PT DOMAIN 396 435 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT	PT REPEAT 439 480 LDL-RECEPTOR CLASS B 1.
FT	PT REPEAT 481 524 LDL-RECEPTOR CLASS B 2.
FT	PT REPEAT 525 567 LDL-RECEPTOR CLASS B 3.
FT	PT REPEAT 568 611 LDL-RECEPTOR CLASS B 4.
FT	PT REPEAT 612 654 LDL-RECEPTOR CLASS B 5.
FT	PT REPEAT 655 696 LDL-RECEPTOR CLASS B 6.
FT	PT DOMAIN 702 750 EGF-LIKE 3.
FT	PT DOMAIN 751 799 CLUSTERED C-TYPE GLYCOCARBONS.
FT	PT DOMAIN 832 837 ENDOCYTOSIS SIGNAL (POTENTIAL).
FT	DISULFID 833 837 BY SIMILARITY.
FT	PT DISULFID 40 58 BY SIMILARITY.
FT	PT DISULFID 52 67 BY SIMILARITY.
FT	PT DISULFID 72 84 BY SIMILARITY.
FT	PT DISULFID 79 97 BY SIMILARITY.
FT	PT DISULFID 91 108 BY SIMILARITY.
FT	PT DISULFID 113 127 BY SIMILARITY.
FT	PT DISULFID 120 140 BY SIMILARITY.
FT	PT DISULFID 134 149 BY SIMILARITY.
FT	PT DISULFID 154 166 BY SIMILARITY.
FT	PT DISULFID 161 179 BY SIMILARITY.
FT	PT DISULFID 173 188 BY SIMILARITY.
FT	PT DISULFID 193 205 BY SIMILARITY.
FT	PT DISULFID 200 218 BY SIMILARITY.
FT	PT DISULFID 212 229 BY SIMILARITY.
FT	PT DISULFID 239 251 BY SIMILARITY.



FT DISULFID 246 264 BY SIMILARITY.  
 FT DISULFID 258 273 BY SIMILARITY.  
 FT DISULFID 278 290 BY SIMILARITY.  
 FT DISULFID 285 303 BY SIMILARITY.  
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 FT DISULFID 326 344 BY SIMILARITY.  
 FT DISULFID 338 355 BY SIMILARITY.  
 FT DISULFID 360 371 BY SIMILARITY.  
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 FT DISULFID 382 394 BY SIMILARITY.  
 FT DISULFID 400 410 BY SIMILARITY.  
 FT DISULFID 406 419 BY SIMILARITY.  
 FT DISULFID 421 434 BY SIMILARITY.  
 FT DISULFID 706 719 BY SIMILARITY.  
 FT DISULFID 715 734 BY SIMILARITY.  
 FT DISULFID 736 749 BY SIMILARITY.  
 FT DISULFID 151 151 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 765 765 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 781 781 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SQUINONE 873 AA: 46280 MM: 016441241A4833 CP064.

Query Match 17.0% Score 82.5; DB 1; Length 873;  
 Best Local Similarity 31.7% Pred No. 0.59;  
 Matches 26; Conservative 7; Mismatches 38; Indels 11; Gaps 4.

QY 5 GGENEKYDS-----GSKED-DKCKYDVEEDDEPNPCIVKCHOD-CVCE 54  
 DB 298 GCPSPVHTHTFASH GHTSTHRSWPTGAGGKLSNGVYTCFTCTGCPFD 287  
 QY 55 GGYRKKDKVSARHEDLNDMD 76  
 DB 298 GSHHSPPGNDIPG-VDNSP 408

RESULT 13  
 LIVER\_RAT STD:RAT PRG: 873 AA.  
 AC P96166;  
 DI 01-OCT-1996 (Ref. 34, Created)  
 DI 01-OCT-1996 (Ref. 34, Last sequence update)  
 DI 01-OCT-2000 (Ref. 40, Last annotation update)  
 DE VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PHORBOL- (VLDL RECEPTOR).  
 GN VLDLR.  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Granata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;  
 CC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC IL2SDE-BIOL;  
 RX MEDLINE=45014480; PubMed=7929662;  
 RA Johnson F V, Landschulz P T, Wynn K L, Ho Y K, Fryman P K.  
 RA Hobbs H H.  
 RT Regulation of the very low density lipoprotein receptor by thyroid  
 RT hormone in rat skeletal muscle.\*  
 RT J Biol Chem 269(26):1-26418(1994)  
 CC -1- FUNCTION: BINDS VLDL AND TRANSPORTS IT INTO CELLS BY ENDOCYTOSIS.  
 CC IN ORDER TO BE INTERNALIZED, THE RECEPTOR-LIGAND COMPLEXES MUST  
 CC FIRST CLUSTER INTO CLATHRIN-COATED PITS.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: ABUNDANT IN SOLEUS, GASTROCNEMIUS, HEART  
 CC MUSCLE, PLACENTA, BRAIN, LUNG AND WHITE FAT. LESS IN ADIP, OVARY,  
 CC KIDNEY, SPLEEN, ADRENAL GLAND, AND THYMUS.  
 CC -1- SIMILARITY: CONTAINS 8 LDL-RECEPTOR CLASS A DOMAINS  
 CC -1- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way

CC Modified and this statement is not covered. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isdb.ch/announcements>  
 CC or send an email to [license@isdb.ch](mailto:license@isdb.ch)).  
 CC -----  
 CC EMBL: L35767; AAA42341.1;  
 CC HSSP: P01130; IAUJ.  
 DR InterPro: IPR000033;  
 DR InterPro: IPR000152;  
 DR InterPro: IPR000561;  
 DR InterPro: IPR001881;  
 DR InterPro: IPR02172;  
 DR Pfam: PF00057; 1dl\_recept; 8.  
 DR Pfam: PF00058; 1dl\_recept; 5.  
 DR PRINTS: PR00261; LDLRECEPTOR.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 2.  
 DR PROSITE: PS00022; EGF\_1; FALSE\_NEG.  
 DR PROSITE: PS01186; EGF\_2; 3.  
 DR PROSITE: PS01187; EGF\_CA; 1.  
 DR PROSITE: PS01204; LDLRA\_1; 8.  
 DR PROSITE: PS00068; LDLRA\_2; 8.  
 DR Clustal: VLDL, Cholesterol metabolism; Lipid transport;  
 KW Endocytosis; Coated pits; Transmembrane; Receptor; Signal;  
 KW EGF-like domain; Repeat.  
 FT SIGNAL 1 27  
 FT CHAIN 28 873  
 FT TRANSMEM 798 873  
 FT DOMAIN 820 819  
 FT DOMAIN 31 69  
 FT DOMAIN 70 130  
 FT DOMAIN 111 151  
 FT DOMAIN 152 190  
 FT DOMAIN 191 231  
 FT DOMAIN 237 275  
 FT DOMAIN 276 314  
 FT DOMAIN 316 355  
 FT DOMAIN 356 395  
 FT DOMAIN 396 435  
 FT REPEAT 439 480  
 FT REPEAT 481 524  
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 FT REPEAT 655 696  
 FT DOMAIN 702 750  
 FT DOMAIN 751 790  
 FT DOMAIN 832 837  
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 FT DISULFID 246 264  
 FT DISULFID 258 273  
 FT DISULFID 278 290  
 FT DISULFID 285 303  
 FT DISULFID 297 312  
 FT DISULFID 318 331  
 FT DISULFID 326 344  
 FT DISULFID 338 355  
 FT DISULFID 360 371  
 FT DISULFID 367 380









US-09-498-556-59

Query Match: 100.0% Score 486; DB 2; Length 84;

Post Local Similarity 100.0% Prod. No. 2,26-43; Index 0; Gaps 0;

Matches 84; Conservative 0; Mismatch 0; Indels 0; Gaps 0;

1 KATMOGENEKENYKOSKEDJOKKXVEEVEEEDDEPWCTVWVTHQVWVEEVEEENK 60  
 1 KATMOGENEKENYKOSKEDJOKKXVEEVEEEDDEPWCTVWVTHQVWVEEVEEENK 60  
 1 KATMOGENEKENYKOSKEDJOKKXVEEVEEEDDEPWCTVWVTHQVWVEEVEEENK 60

61 DOKVSAWETELNMDFTYVSTEN 84  
 61 DOKVSAWETELNMDFTYVSTEN 84  
 61 DOKVSAWETELNMDFTYVSTEN 84

RESULT 2  
 US-09-498-556-59  
 Section 59; Application 09/08/486-59  
 Patent No. 586542

GENERAL INFORMATION:  
 APPLICANT: George P. Vlasak, Patrick H. Stansons,  
 APPLICANT: Joris H.L. Meunier, Marc J. Lauroys,  
 APPLICANT: Yves R. Laroche, Laurent St. Josephs,  
 APPLICANT: Yvanick G.J. Gaussemans, Matthew Moylo,  
 APPLICANT: Peter W. Bequam

TITLE OF INVENTION: MEMBRANE-EXTRACTED ANTI-AGGLUTININ  
 NUMBER OF INVENTORS: FIVE  
 NUMBER OF STUDENTS: 47

CORRESPONDENT ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 644 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.

ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 4.5" Diskette, 1.44 MB  
 MEDIUM TYPE: Storage  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: IBM PC, DOS 5.0

SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 FILING DATE: October 19, 1994  
 FILING DATE: June 5, 1995  
 FILING DATE: June 5, 1995

REGISTRATION NUMBER: 40,158  
 REGISTRATION NUMBER: 40,158  
 REGISTRATION NUMBER: 40,158  
 REGISTRATION NUMBER: 40,158  
 REGISTRATION NUMBER: 40,158

TELEPHONE: (213) 489-1600  
 TELEPHONE: (213) 489-1600  
 TELEPHONE: (213) 489-1600  
 TELEPHONE: (213) 489-1600  
 TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440  
 TELEFAX: (213) 955-0440  
 TELEFAX: (213) 955-0440  
 TELEFAX: (213) 955-0440  
 TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 59:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 84 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Ancylostoma caninum

US-09-498-556-59

Query Match: 100.0% Score 486; DB 2; Length 84;

Post Local Similarity 100.0% Prod. No. 2,26-43; Index 0; Gaps 0;

Matches 84; Conservative 0; Mismatch 0; Indels 0; Gaps 0;

1 KATMOGENEKENYKOSKEDJOKKXVEEVEEEDDEPWCTVWVTHQVWVEEVEEENK 60  
 1 KATMOGENEKENYKOSKEDJOKKXVEEVEEEDDEPWCTVWVTHQVWVEEVEEENK 60  
 1 KATMOGENEKENYKOSKEDJOKKXVEEVEEEDDEPWCTVWVTHQVWVEEVEEENK 60

61 DOKVSAWETELNMDFTYVSTEN 84  
 61 DOKVSAWETELNMDFTYVSTEN 84  
 61 DOKVSAWETELNMDFTYVSTEN 84

RESULT 3  
 US-09-498-556-59  
 Section 59; Application 09/08/486-59  
 Patent No. 586542

GENERAL INFORMATION:  
 APPLICANT: George P. Vlasak, Patrick H. Stansons,  
 APPLICANT: Joris H.L. Meunier, Marc J. Lauroys,  
 APPLICANT: Yves R. Laroche, Laurent St. Josephs,  
 APPLICANT: Yvanick G.J. Gaussemans, Matthew Moylo,  
 APPLICANT: Peter W. Bequam

TITLE OF INVENTION: MEMBRANE-EXTRACTED ANTI-AGGLUTININ  
 NUMBER OF INVENTORS: FIVE  
 NUMBER OF STUDENTS: 47

CORRESPONDENT ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 644 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.

ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 4.5" Diskette, 1.44 MB  
 MEDIUM TYPE: Storage  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: IBM PC, DOS 5.0

SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 FILING DATE: October 19, 1994  
 FILING DATE: June 5, 1995  
 FILING DATE: June 5, 1995

REGISTRATION NUMBER: 40,158  
 REGISTRATION NUMBER: 40,158  
 REGISTRATION NUMBER: 40,158  
 REGISTRATION NUMBER: 40,158  
 REGISTRATION NUMBER: 40,158

TELEPHONE: (213) 489-1600  
 TELEPHONE: (213) 489-1600  
 TELEPHONE: (213) 489-1600  
 TELEPHONE: (213) 489-1600  
 TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440  
 TELEFAX: (213) 955-0440  
 TELEFAX: (213) 955-0440  
 TELEFAX: (213) 955-0440  
 TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 59:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 84 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Ancylostoma caninum

US-09-498-556-59

Query Match: 100.0% Score 486; DB 2; Length 84;

Post Local Similarity 100.0% Prod. No. 2,26-43; Index 0; Gaps 0;

Matches 84; Conservative 0; Mismatch 0; Indels 0; Gaps 0;

1 KATMOGENEKENYKOSKEDJOKKXVEEVEEEDDEPWCTVWVTHQVWVEEVEEENK 60  
 1 KATMOGENEKENYKOSKEDJOKKXVEEVEEEDDEPWCTVWVTHQVWVEEVEEENK 60  
 1 KATMOGENEKENYKOSKEDJOKKXVEEVEEEDDEPWCTVWVTHQVWVEEVEEENK 60

61 DOKVSAWETELNMDFTYVSTEN 84  
 61 DOKVSAWETELNMDFTYVSTEN 84  
 61 DOKVSAWETELNMDFTYVSTEN 84

RESULT 3  
 US-09-498-556-59  
 Section 59; Application 09/08/486-59  
 Patent No. 586542

GENERAL INFORMATION:  
 APPLICANT: George P. Vlasak, Patrick H. Stansons,  
 APPLICANT: Joris H.L. Meunier, Marc J. Lauroys,  
 APPLICANT: Yves R. Laroche, Laurent St. Josephs,  
 APPLICANT: Yvanick G.J. Gaussemans, Matthew Moylo,  
 APPLICANT: Peter W. Bequam

TITLE OF INVENTION: MEMBRANE-EXTRACTED ANTI-AGGLUTININ  
 NUMBER OF INVENTORS: FIVE  
 NUMBER OF STUDENTS: 47

CORRESPONDENT ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 644 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.

ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 4.5" Diskette, 1.44 MB  
 MEDIUM TYPE: Storage  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: IBM PC, DOS 5.0

SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 FILING DATE: October 19, 1994  
 FILING DATE: June 5, 1995  
 FILING DATE: June 5, 1995

REGISTRATION NUMBER: 40,158  
 REGISTRATION NUMBER: 40,158  
 REGISTRATION NUMBER: 40,158  
 REGISTRATION NUMBER: 40,158  
 REGISTRATION NUMBER: 40,158

TELEPHONE: (213) 489-1600  
 TELEPHONE: (213) 489-1600  
 TELEPHONE: (213) 489-1600  
 TELEPHONE: (213) 489-1600  
 TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440  
 TELEFAX: (213) 955-0440  
 TELEFAX: (213) 955-0440  
 TELEFAX: (213) 955-0440  
 TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 59:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 84 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Ancylostoma caninum

US-09-498-556-59

Query Match: 100.0% Score 486; DB 2; Length 84;

Post Local Similarity 100.0% Prod. No. 2,26-43; Index 0; Gaps 0;

Matches 84; Conservative 0; Mismatch 0; Indels 0; Gaps 0;

1 KATMOGENEKENYKOSKEDJOKKXVEEVEEEDDEPWCTVWVTHQVWVEEVEEENK 60  
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61 DOKVSAWETELNMDFTYVSTEN 84  
 61 DOKVSAWETELNMDFTYVSTEN 84  
 61 DOKVSAWETELNMDFTYVSTEN 84

## RESULT 4

US-09-461-965-59

Sequence 59 Application no:09841045

Patient No. 582098

## GENERAL INFORMATION:

APPLICANT: GEORGE P. VIASUK, PATRIC H. STANSENS,  
 APPLICANT: Joris H.L. Meunens, Marc J. Lauwereys,  
 APPLICANT: Yves R. Lathuere, Laurent S. Jaspers,  
 APPLICANT: Vanlier G.J. Gansmaes, Mathew Moylo,  
 APPLICANT: Peter W. Bergum  
 TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
 NUMBER OF INVENTION: FR-0111  
 NUMBER OF SEQUENCES: 356  
 ADDRESS/PHONE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 643 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
 MEDIUM TYPE: Storage  
 OPERATING SYSTEM: IBM Compatible  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 FILING DATE: April 19, 1996  
 FILING DATE: October 17, 1995  
 CLASSIFICATION: 59

## PRIOR APPLICATION DATA:

ATTORNEY/AGENT NUMBER: 06/486, 897  
 FILING DATE: October 18, 1994

## ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/SECRET NUMBER: 06/461, 965  
 FILING DATE: June 5, 1995

## TELEPHONE: (213) 489-1600

TELEPHONE: (213) 489-0440

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TELEPHONE: (213) 489-0440

US-09-461-965-59

Query Match: 100.0% Score 486; DB 2; Length 84;

Best local Similarity: 100.0%; Pred. No. 2,2e-43;

Mismatch: 0; Indels: 0; Gaps: 0;

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DB 1 FAIRLY ACCURATE MATCH: 100.0% Score 486; DB 2; Length 84;

DB 1 FAIRLY ACCURATE MATCH: 100.0% Score 486; DB 2; Length 84;

DB 1 FAIRLY ACCURATE MATCH: 100.0% Score 486; DB 2; Length 84;

APPLICANT: VIASUK, George P. VIASUK

APPLICANT: Stanssens, Patrick Eric Hugo

APPLICANT: Meunens, Joris Hilda Lieven

APPLICANT: Lauwereys, Marc Joset

APPLICANT: Lathuere, Yves Rene

APPLICANT: Jaspers, Laurent Stephane

APPLICANT: Gansmaes, Vanlier G.J. Georges Jozet

APPLICANT: Moylo, Mathew

APPLICANT: Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT

NUMBER OF INVENTION: FR-0111

NUMBER OF SEQUENCES: 356

ADDRESS/PHONE ADDRESS:

ADDRESSEE: Lyon &amp; Lyon

STREET: 643 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

MEDIUM TYPE: Storage

OPERATING SYSTEM: IBM Compatible

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

FILING DATE: April 19, 1996

FILING DATE: October 17, 1995

CLASSIFICATION: 59

PRIOR APPLICATION DATA:

ATTORNEY/AGENT NUMBER: 06/486, 897

FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REFERENCE/SECRET NUMBER: 06/461, 965

FILING DATE: June 5, 1995

TELEPHONE: (213) 489-1600

TELEPHONE: (213) 489-0440

TELEPHONE: (213) 489-0440

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TELEPHONE: (213) 489-0440

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TELEPHONE: (213) 489-0440

TELEPHONE: (213) 489-0440

US-09-644-641-59

Query Match: 100.0% Score 156; DB 2; Length 84;

Best local Similarity: 100.0%; Pred. No. 2,2e-43;

Mismatch: 0; Indels: 0; Gaps: 0;

DB 1 FAIRLY ACCURATE MATCH: 100.0% Score 156; DB 2; Length 84;

DB 1 FAIRLY ACCURATE MATCH: 100.0% Score 156; DB 2; Length 84;

DB 1 FAIRLY ACCURATE MATCH: 100.0% Score 156; DB 2; Length 84;

DB 1 FAIRLY ACCURATE MATCH: 100.0% Score 156; DB 2; Length 84;

DB 1 FAIRLY ACCURATE MATCH: 100.0% Score 156; DB 2; Length 84;

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DB 1 FAIRLY ACCURATE MATCH: 100.0% Score 156; DB 2; Length 84;









[illegible]

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1 ZIP: 90071
2 COMPUTER RELEASABLE FORM:
3 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
4 MEDIUM TYPE: Storage
5 MEDIUM TYPE: Compact Disk
6 OPERATING SYSTEM: IBM P.C., DOS 5.0
7 SOFTWARE: Word Perfect 5.1
8 CHECKED ATTENTION DATA:
9 ALLOCATION NUMBER: 50739765, 380
10 FILING DATE: June 5, 1994
11 CLASSIFICATION: 540
12 FOR ALLOCATION DATA:
13 ATTENTION NUMBER: 087456, 110
14 FILING DATE: October 18, 1994
15 ACTION/TITLE INFORMATION:
16 NAME: William S. GARRA L.
17 REGISTRATION NUMBER: 40,158
18 REFERENCE: Vol. NUMBER: 213, 268
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: (213) 489-1600
21 TELEFAX: (213) 955-0440
22 TELEX: 47-3510
23 INFORMATION FOR STD. ID NO.: 128:
24 SEQUENCE CHARACTERISTICS:
25 LENGTH: 91 amino acids
26 TYPE: amino acid
27 TOPOLOGY: linear
28 MOLECULE TYPE: peptide
29 ORIGINAL SOURCE:
30 ORGANISM: Anystola caninum
31 US-08-465-460-128
32
33 Query Match 100.0% Score 486; DB 2; Length 91;
34 Best Local Similarity 100.0%; Pred. No. 2,46 43;
35 Matches 84; Conservative 0; Mismatches 0; Indels 0; Caps 0
36
37 1 PATENT INFORMATION: YES=YES,NO=NO,LV=LVS,VLEV=LEV,VTE=TEP,NK=NK,
38 8 PAIRED=PAIRS,DNA=DNA,RN=RN,VIR=VIR,PEP=PEP,VAL=VAL,CHEM=CHEM,VOL=VOL,REF=REF,
39 |||||||
40 61 DECVSAPELMDNMDFITGTEN 84
41 |||||||
42 DB 68 DRCVSAHRLDLMDFITGTEN 91
43
44 RESULT 13
45 US-08-480-478-50
46 Sequence 59; Application US/09480478
47 Patent No. 5864009
48 SERIAL INFORMATION:
49 APPLICANT: GEORGE P. VLASTIK; PATRICK ERIC
50 APPLICANT: HUGO STANISINSKI; JORDIS HILDA
51 APPLICANT: LEEVER NISSING; MARC JOZEF
52 APPLICANT: LAURENTS; YVES BERNI LAROCHE
53 APPLICANT: LAURENT STEPHANE JESPERE; and
54 APPLICANT: VANNUCK GEORGES JOSEF
55 APPLICANT: CARSTENS
56 TITLE OF INVENTION: REAGENTS, EXTRACTED ANTI-
57 TIBER OF INVENTION: CANDIDATE PROTEIN
58 NUMBER OF SEQUENCES: 86
59 ADDRESS/CLIENT ADDRESS:
60 ADDRESSEE: Lyon & Lyon
61 STREET: 613 West Fifth Street
62 STREET: Suite 4700
63 CITY: Los Angeles
64 STATE: California
65 COUNTRY: U.S.A.
66 ZIP: 90071
67
68 COMPUTER RELEASABLE FORM:
69 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
70 MEDIUM TYPE: Storage
71 COMPUTER: IBM Compact Disk

```

APPROVAL: 08/26/10  
 FILED DATE: October 18, 1994  
 APPROVED/AGENT: [Signature]

TELLEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
E-MAIL: 67-4510

# INFORMATION FOR SEQ ID NO: 128:

SEQUENCE CHARACTERISTICS:

LENGTH: 91 amino acids

TYPE: amino acid

TOPOLOGY: 1 loop

MOLWEIGHT TYPE: 10000

ORGANISM SOURCE:

ORGANISM: Anoxyplasma caninum

US-09-498-556-128

Query Match: 100.0%; Score: 486; 108.2; Length: 91;

Best Local Similarity: 100.0%; Prod. No. 2.4e-43;

Matches: 84; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

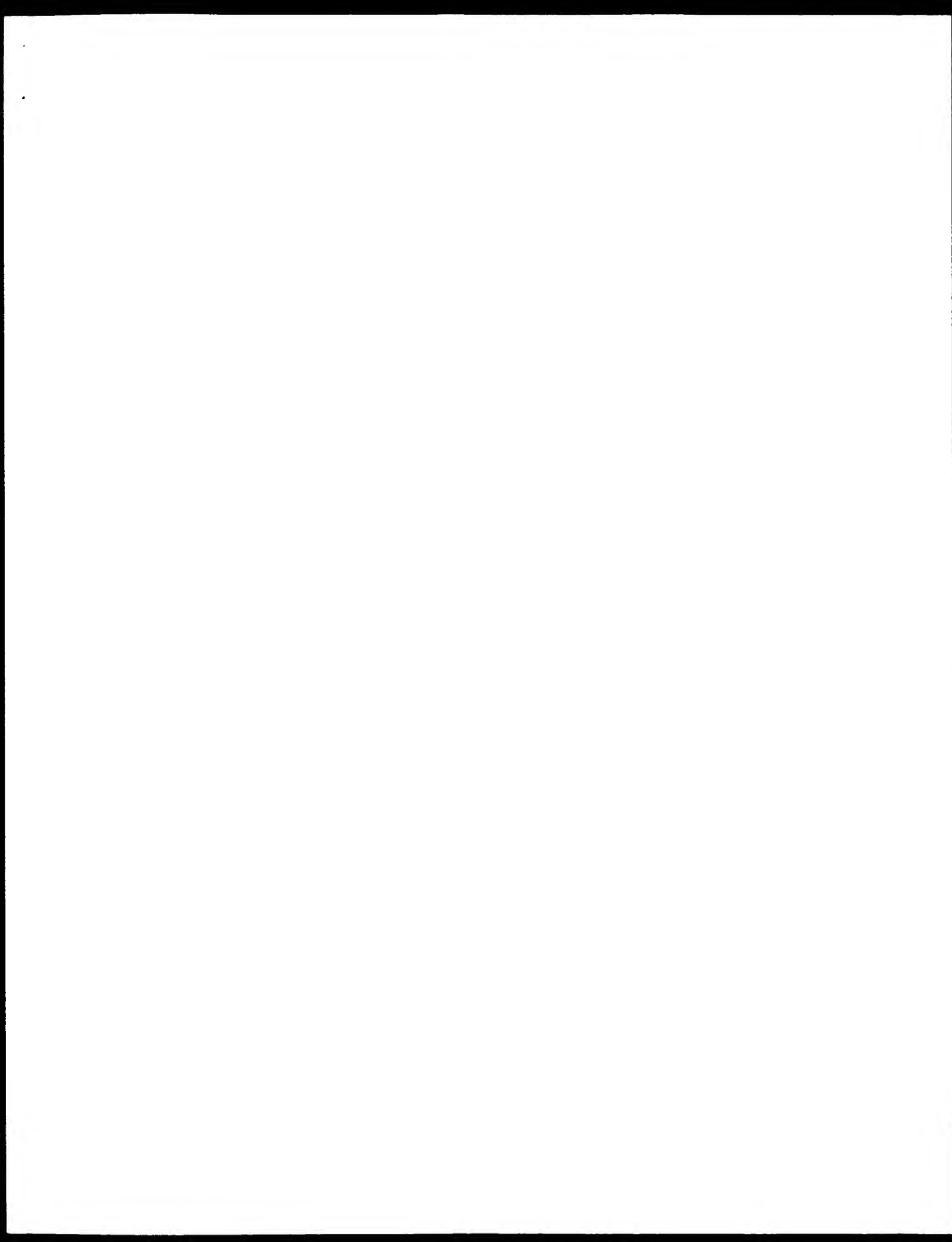
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QY 61 DDKCVSAEDPELNMDETPGIRN 84

10 68 DDKCVSAEDPELNMDETPGIRN 91

Search completed: September 30, 2001, 10:29:37  
Job time: 47 sec











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10 01 MAY 2001 (TREMBLER: 16, last sequence update)
11 01 MAR 2001 (TREMBLER: 16, last annotation update)
12 YOUNG 38 PROTEIN.
13 YOUNG 38.
14 CAPORELLI 11.
15 CAPORELLI 11.
16 Eukaryota: Metazoa: Nemertea: Chromadorea: Rhadaliidae: Rhadaliidae
17 Rhadaliidae: Polidoriinae: Caporellididae.
18 NCBI TaxID 62393.
19 111.
20 SEQUENCE FROM N.A.
21 MONTAGNA A.A.
22 SEQUENCE FROM N.A.
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10 01 MAY 2001 (TREMBLER: 16, last sequence update)
11 01 MAR 2001 (TREMBLER: 16, last annotation update)
12 YOUNG 38 PROTEIN.
13 YOUNG 38.
14 CAPORELLI 11.
15 CAPORELLI 11.
16 Eukaryota: Metazoa: Nemertea: Chromadorea: Rhadaliidae: Rhadaliidae
17 Rhadaliidae: Polidoriinae: Caporellididae.
18 NCBI TaxID 62393.
19 111.
20 SEQUENCE FROM N.A.
21 MONTAGNA A.A.
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99 SEQUENCE FROM N.A.
100 SEQUENCE FROM N.A.

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10 519. ENHANCED PROSPECTING TWO-STEP METHOD  
 25 61. DISCOVERY 71  
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 40 474 ENHANCED 684  
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AA		674933;
D1	01-NA-1959 (THERMOL), 12, created)	
D1	01-NA-1959 (THERMOL), 12, last sequence update)	
D1	01-MAV-2001 (THERMOL), 19, last annotation update)	
D1E	ZBRACHESIN (THERMOL);	
OS	Homo sapiens (human);	
ORG	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;	
OX	[taxid:9606];	
K0		SEQUENCE FROM N.A.
KA	Glaucopneustes, Krasnodar A., Scherzer S., Weber J., Schatzberg R.,	
RA	Istail L., C.;	
R1	"Large scale analysis of two regions in human chromosome 7q22:	
R1	annotation of 970 kb of genomic sequence around the POU3F1 and CTNLL1	
R1	loci reveals 17 genes."	
R1	Submitted (MAV 1945) to the GenBank database by Glaucoptes,	
R8	EMBL: AF053355, AAC76790.1 ;	
D8	TatCtPro; IP80010615 ; -	
D8	TatCtPPro; IP8040998 ; -	
D8	TatCtPPro; IP8001445 ; -	
D8	TatCtPPro; IP8002919 ; -	
D8	TatCtPPro; IP8002965 ; -	
D8	Pfam: PF00994; 9841: 4;	
D8	Pfam: PF00629; MAM_3;	
D8	Pfam: PF01826; 111: 4;	
D8	Pfam: PF02445; 1114: 4;	
D8	FTHS; F801217; FRICHTEXTEN;	
D8	PROSITE: PS01195; EST_2; ORKN.WN_3;	
D8	PROSITE: PS00740; MAM_1; 1;	
D8	SMART: SM00216; VIM_1;	
D8	PROLIR 2776 2776	
D8	SEQUENCE 2 479 AA: 257820 MW: 6900024.41673940 PK%54;	

[illegible]

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